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Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's
Name:

BASKAR

Serial
Number:

10010160

Date:

9/30/03

Phone:

308-8886

Art Unit:

1645

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Claims 22-24

30-33

37-50

Seq. LD. No. 1

NA

Lign

Interferon
40 kb

Search:

NM 0016477

Accession rules

Lawsonia Intracellular
Vaccine

BEST AVAILABLE COPY

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Date completed:

10-08-03

Searcher:

Beverly C 4974

Terminal time:

20 / 10

Elapsed time:

CPU time:

Total time:

25 / 22

Number of Searches:

Number of Databases:

2

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other CGN

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Baskar P.
10/010160

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(FILE 'HCAPLUS' ENTERED AT 12:36:01 ON 08 OCT 2003)

L1 103 SEA FILE=HCAPLUS ABB=ON PLU=ON (LAWSON? OR L) (W) INTRACE
LL?

L2 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 AND (FLHB OR FLH B
OR PGTE? OR 16477)

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:368499 HCAPLUS

DOCUMENT NUMBER: 136:382847

TITLE: Genes for antigenic proteins of Lawsonia and
their use diagnosis and prophylaxis of Lawsonia
infection

INVENTOR(S): Rosey, Everett Lee; King, Kendall Wayne; Good,
Robert Trygve; Strugnell, Richard Anthony

PATENT ASSIGNEE(S): Agriculture Victoria Services Pty. Ltd.,
Australia; Australian Pork Limited; Pfizer
Products, Inc.

SOURCE: PCT Int. Appl., 155 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002038594	A1	20020516	WO 2001-AU1462	20011109
WO 2002038594	C2	20021107		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
AU 2002014810	A5	20020521	AU 2002-14810	20011109
US 2003103999	A1	20030605	US 2001-10160	20011109
BR 2001014835	A	20030701	BR 2001-14835	20011109
EP 1332154	A1	20030806	EP 2001-983297	20011109
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
PRIORITY APPLN. INFO.:			AU 2000-1381	A 20001110
			US 2000-249596P	P 20001117
			WO 2001-AU1462	W 20011109

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganisms. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis**, which encodes an immunogenic polypeptide that is particularly useful as an antigen in a vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts, wherein said polypeptide is

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selected from the group consisting of **flhB**, **fliR**, **ntnC**, **glnH**, **motA**, **motB**, **tlyC**, **ytfM**, and **ytfN** polypeptides, or a homolog, analog or derivative of any one or more of said polypeptides. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:37:32 ON 08 OCT 2003)

L3

1 S L2

L3 ANSWER 1 OF 1 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2002-557448 [59] WPIDS

DOC. NO. NON-CPI: N2002-441304

DOC. NO. CPI: C2002-158153

TITLE: New immunogenic polypeptide comprising epitope of *Lawsonia* spp. polypeptide such as **flhB**, **fliR**, **ntnC**, **glnH**, **motA**, polypeptides, useful in vaccines for treatment of porcine proliferative enteropathy in pigs and birds.

DERWENT CLASS: B04 C06 D16 S03

INVENTOR(S): GOOD, R T; KING, K W; LEEROSEY, E; STRUGNELL, R A; ROSEY, E L

PATENT ASSIGNEE(S): (AGRI-N) AGRIC VICTORIA SERVICES PTY LTD; (AUPO-N) AUSTRALIAN PORK LTD; (PFIZ) PFIZER PROD INC; (GOOD-I) GOOD R T; (KING-I) KING K W; (ROSE-I) ROSEY E L; (STRU-I) STRUGNELL R A

COUNTRY COUNT: 99

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002038594	A1	20020516	(200259)*	EN	155
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC					
MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ					
DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP					
KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ					
NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA					
UG US UZ VN YU ZA ZW					
AU 2002014810	A	20020521	(200260)		
US 2003103999	A1	20030605	(200339)		
EP 1332154	A1	20030806	(200353)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK					
NL PT RO SE SI TR					
BR 2001014835	A	20030701	(200356)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002038594	A1	WO 2001-AU1462	20011109
AU 2002014810	A	AU 2002-14810	20011109

Searcher : Shears 308-4994

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10/010160

US 2003103999 A1 Provisional	US 2000-249595P	20001117
	US 2001-10160	20011109
EP 1332154 A1	EP 2001-983297	20011109
	WO 2001-AU1462	20011109
BR 2001014835 A	BR 2001-14835	20011109
	WO 2001-AU1462	20011109

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002014810 A	Based on	WO 2002038594
EP 1332154 A1	Based on	WO 2002038594
BR 2001014835 A	Based on	WO 2002038594

PRIORITY APPLN. INFO: US 2000-249596P 20001117; AU 2000-1381
20001110

AN 2002-557448 [59] WPIDS

AB WO 200238594 A UPAB: 20020916

NOVELTY - An isolated or recombinant immunogenic polypeptide (I) which comprises, mimics or cross-reacts with a B-cell or T-cell epitope of a Lawsonia spp. polypeptide such as fihB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM or ytfN polypeptides, is new.

DETAILED DESCRIPTION - An isolated or recombinant immunogenic polypeptide (I) which comprises, mimics or cross-reacts with a B-cell or T-cell epitope of a Lawsonia spp. polypeptide such as fihB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM or ytfN polypeptides, is:

(i) a polypeptide of Lawsonia spp. which comprises an amino acid sequence that has at least about 60% sequence identity overall to a fully defined amino acid (PS) sequence of 207 (S2), 262 (S4), 456 (S6), 137 (S8), 282 (S10), 237 (S12), 348 (S14), 602 (S16), or 1382 (S18) amino acids as given in specification;

(ii) a polypeptide of Lawsonia spp. which comprises an amino acid sequence which has at least 60% sequence identity overall to an amino acid sequence encoded by *L. intracellularis*

(Li) DNA contained within a plasmid (P) having AGAL Accession Nos:

NM00/16476 (plasmid **pGTE1** glnH); NM00/16477

(plasmid **pGTE2** flhB); NM00/16478 (plasmid

pGTE3 fliR); NM00/16479 (plasmid **pGTE4** motA/B);

NM00/16480 (plasmid **pGTE5** tlyC); NM00/16481 (plasmid

pGTE6 ntrC); NM00/16482 (plasmid **pGTE7** ytfM); or

NM01/23286 (plasmid **pGTE8** ytfN);

(iii) a polypeptide which comprises at least about 5 contiguous amino acids of PS;

(iv) a polypeptide which comprises at least about 5 contiguous amino acids of amino acid sequence of Li DNA contained within (P);

(v) a polypeptide which comprises an amino acid sequence encoded by nucleotide sequence of Lawsonia spp. having at least 60% identity overall to a fully defined nucleotide sequence (NS) of 622 (S1), 789 (S3), 1371 (S5), 412 (S7), 849 (S9), 717 (S11), 1047 (S13), 1812 (S15), or 4149 (S17) nucleotides as given in specification;

(vi) a polypeptide which comprises an amino acid sequence encoded by a nucleotide sequence of Lawsonia spp. having at least 60% sequence identity overall to nucleotide sequence of Li DNA contained with an (P);

(vii) a polypeptide encoded by at least 15 contiguous

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nucleotides of NS;

(viii) a polypeptide encoded by at least 15 contiguous nucleotides of nucleotide sequence of Li DNA contained within (P); or

(ix) a homolog, analog or derivative of above mentioned polypeptides which mimic a B-cell or T-cell epitope of *Lawsonia* spp.

INDEPENDENT CLAIMS are also included for the following:

(1) a vaccine composition (II) for the prophylaxis or treatment of infection of an animal by *Lawsonia* spp. which comprises an immunogenic component that comprises (I) and one or more carriers, diluents or adjuvants suitable for veterinary or pharmaceutical use;

(2) a combination vaccine composition (III) for the prophylaxis or treatment of infection of an animal by *Lawsonia* spp., comprising:

(i) a first immunogenic component which comprises (I); and

(ii) a second immunogenic component different from first immunogenic component and comprising a Li polypeptide such as FlgE, hemolysin, OmpH, SodC, **flhB**, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, or ytfN polypeptides and one or more carriers, diluents or adjuvants suitable for veterinary or pharmaceutical use;

(3) a vaccine vector (IV) that comprises, in an expressible form, an isolated nucleic acid molecule (V) comprising a nucleotide sequence such as:

(i) a protein-encoding nucleotide sequence having at least 60% sequence identity overall to a sequence of NS;

(ii) a protein-encoding nucleotide sequence having at least 60% identity overall to the protein-encoding sequence of Li DNA contained within (P);

(iii) a protein-encoding nucleotide sequence which comprises at least about 15 contiguous nucleotides of NS;

(iv) a protein-encoding nucleotide sequence which comprises at least 15 contiguous nucleotides of Li DNA contained within (P);

(v) a protein-encoding nucleotide sequence which hybridizes under low stringency condition to the complement of NS;

(vi) a protein-encoding nucleotide sequence which hybridizes under low stringency conditions to non-coding strand of Li DNA contained within (P); and

(vii) a homolog, analog or derivative of above mentioned nucleotide sequences which encodes the polypeptide that mimics a B-cell or T-cell epitope of *Lawsonia* spp.;

(4) an isolated polyclonal or monoclonal antibody molecule (VI) that binds specifically to *Lawsonia* spp. polypeptide of **flhB**, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, or ytfN polypeptide, or homolog, analog or derivative of the above mentioned polypeptide;

(5) an isolated nucleic acid molecule (N) which consists of a nucleotide sequence encoding *Lawsonia* spp. such as **flhB**, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, or ytfN;

(6) a probe or primer comprising any one of fully defined 50 oligonucleotide sequences as given in specification such as catattcaaggtacagcatctgatgg, ctctttacaaaccttgctcc, gctcatctaaagaacactttcc, caaggtagtatacaacttattgg, etc., or complementary nucleotide sequence to the oligonucleotide sequence;

(7) a plasmid having AGAL Accession Nos: NM00/16476 (plasmid **pGTE1** glnH); NM00/16477 (plasmid **pGTE2** **flhB**); NM00/16478 (plasmid **pGTE3** fliR); NM00/16479 (plasmid **pGTE4** motA/B); NM00/16480 (plasmid **pGTE5** tlyC); NM00/16481 (plasmid **pGTE6** ntrC); NM00/16482 (plasmid **pGTE7** ytfM); or NM01/23286 (plasmid **pGTE8**

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ytfn);

(8) a recombinant vector (VII) capable of replication in a host cell, where the vector comprises (N);

(9) a host cell (VIII) comprising (VII);

(10) identifying (M1) whether or not a porcine or avian animal has suffered from a past infection, or is currently infected, with Li or a microorganism that is immunologically cross-reactive with Li;

(11) diagnosing (M2) infection of a porcine or avian animal by Li or a microorganism that is immunologically cross-reactive with Li; and

(12) detecting (M3) Li or related microorganism in a biological sample derived from a porcine or avian animal subject.

ACTIVITY - Antibacterial.

MECHANISM OF ACTION - Vaccine. No supporting data is given.

USE - (I) is useful for identifying whether or not a porcine or avian animal has suffered from a past infection, or is currently infected, with Li or a microorganism that is immunologically cross-reactive with Li. (VI) is useful for diagnosing infection of a porcine or avian animal by Li or a microorganism that is immunologically cross-reactive with Li. (N) is useful as probes or primers for detecting Li or related microorganism in a biological sample derived from a porcine or avian animal subject (all claimed).

(I) is preferably useful for vaccinating porcine animals against porcine proliferative enteropathy (PPE). (I) is also useful in vaccines for the prophylaxis and treatment of PPE in birds. (II) is useful for conferring protection against infection by other species of the genus Lawsonia or other microorganisms related to Li.

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FILE 'HCAPLUS' ENTERED AT 12:38:00 ON 08 OCT 2003

L4 0 S L1 AND NM0016477

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:38:20 ON 08 OCT 2003

L5 0 S L4

(FILE 'HCAPLUS' ENTERED AT 12:38:37 ON 08 OCT 2003)

L1 103 SEA FILE=HCAPLUS ABB=ON PLU=ON (LAWSON? OR L) (W) INTRACE LL?

L6 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 AND (16476 OR GLNH OR GLN H OR FLIR OR FLI R OR 16478 OR 16479 OR MOTA OR MOTB OR MOT OR MOTAB OR 16480 OR TLYC OR (NTR OR TLY) (W)C OR NTRC OR 16482 OR YTFM OR YTF(W) (M OR N) OR YTFN OR 23286)

L7 0 L6 NOT L2

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:42:26 ON 08 OCT 2003)

L8 1 S L6

L9 0 S L8 NOT L3

(FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 12:44:05 ON 08 OCT 2003)

L10 112 S "ROSEY E"?/AU

L11 3959 S "KING K"?/AU

-Author (s)

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10/010160

L12 7205 S "GOOD R"?/AU
L13 386 S "STRUGNELL R"?/AU
L14 2 S L10 AND L11 AND L12 AND L13
L15 14 S L10 AND (L11 OR L12 OR L13)
L16 2 S L11 AND (L12 OR L13)
L17 2 S L12 AND L13
L18 11644 S L10 OR L11 OR L12 OR L13
L19 18 S L18 AND L1
L20 30 S L14 OR L15 OR L16 OR L17 OR L19
L21 16 DUP REM L20 (14 DUPLICATES REMOVED)

L21 ANSWER 1 OF 16 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2003:434075 BIOSIS
DOCUMENT NUMBER: PREV200300434075
TITLE: **Lawsonia intracellularis**
proteins, and related methods and materials.
AUTHOR(S): **Rosey, Everett L.**
ASSIGNEE: Pfizer, Inc.; Pfizer Products, Inc.
PATENT INFORMATION: US 6605696 August 12, 2003
SOURCE: Official Gazette of the United States Patent and
Trademark Office Patents, (Aug. 12 2003) Vol. 1273,
No. 2, pp. No. Pagination.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English

AB Isolated polynucleotide molecules contain a nucleotide sequence that encodes a **L. intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1, or Omp100 protein, a substantial portion of the sequences, or a homologous sequence. Related polypeptides, immunogenic compositions and assays are described.

L21 ANSWER 2 OF 16 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-416977 [39] WPIDS
DOC. NO. CPI: C2003-110367
TITLE: New isolated **Lawsonia intracellularis** polynucleotide and polypeptide, useful for the prevention and diagnosis of Lawsonia infections in susceptible animals, such as pigs.
DERWENT CLASS: B04 C06 D16
INVENTOR(S): **ROSEY, E L**
PATENT ASSIGNEE(S): (ROSE-I) ROSEY E L
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2003021802	A1	20030130	(200339)*		64

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2003021802	A1	Provisional	US 1999-160922P 19991022
		Provisional	US 1999-163858P 19991105
		Cont of	US 2000-689065 20001012

Searcher : Shears 308-4994

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US 2002-210296 20020801

PRIORITY APPLN. INFO: US 2002-210296 20020801; US 1999-160922P
19991022; US 1999-163858P 19991105; US
2000-689065 20001012

AN 2003-416977 [39] WPIDS

AB US2003021802 A UPAB: 20030619

NOVELTY - A new isolated polynucleotide molecule (I) comprises:

(a) a sequence encoding **Lawsonia intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein;

(b) a sequence that is a substantial part of the encoding sequence of (a); or

(c) a sequence homologous to the sequences of (a) or (b).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a polynucleotide molecule comprising a nucleotide sequence greater than 20 nucleotides having promoter activity and found within a fully defined sequence of 5445 bp, given in the specification, from nucleotide 2691-2890, or its complement;

(2) a recombinant vector comprising (I);

(3) a transformed host cell comprising the vector of (2);

(4) a polypeptide produced by the transformed host cell of (3);

(5) a genetic construct comprising a polynucleotide molecule that can be used to alter a **Lawsonia** gene, comprising: (a) polynucleotide molecule comprising a sequence that is otherwise the same as a nucleotide sequence of a htrA, ponA, hypC, lysS, ycfW, abcl or omp100 gene, or its homolog, substantial portion, or mutations capable of altering the above mentioned genes; or (b) a polynucleotide molecule comprising a sequence that naturally flanks in situ the ORF of the htrA, ponA, hypC, lysS, ycfW, abcl or omp100 gene, or its homolog;

(6) a transformed host cell comprising the genetic construct of (5);

(7) an isolated polypeptide comprising: (a) a **Lawsonia intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein; (b) homologs or substantial portions of (a); (c) a fusion protein of the polypeptide in (a) or (b) fused to another protein or polypeptide; or (d) an analog or derivative of the polypeptide in (a), (b) or (c);

(8) a substantially pure polypeptide comprising an epitope of HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein that is specifically reactive with anti-**Lawsonia** antibodies;

(9) an isolated polypeptide comprising the sequence encoded by (I);

(10) an isolated antibody that specifically reacts with **L. intracellularis** HtrA, PonA, HypC, LysS, YcfW, ABC1 or Omp100 protein;

(11) a live attenuated vaccine comprising the transformed cell of (6);

(12) a killed cell vaccine comprising transformed cells of (6) in killed form; and

(13) an immunogenic composition comprising (I) or the polypeptide of (7), in combination with a carrier.

ACTIVITY - Antibacterial. No biological data given.

MECHANISM OF ACTION - Vaccine.

USE - The methods and compositions of the present invention are

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useful for the prevention and diagnosis of **L. intracellularis** infections in susceptible animals, such as pigs.
Dwg.0/9

L21 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 1
ACCESSION NUMBER: 2002:368499 HCAPLUS
DOCUMENT NUMBER: 136:382847
TITLE: Genes for antigenic proteins of Lawsonia and their use diagnosis and prophylaxis of Lawsonia infection
INVENTOR(S): Rosey, Everett Lee; King, Kendall Wayne; Good, Robert Trygve; Strugnell, Richard Anthony
PATENT ASSIGNEE(S): Agriculture Victoria Services Pty. Ltd., Australia; Australian Pork Limited; Pfizer Products, Inc.
SOURCE: PCT Int. Appl., 155 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002038594	A1	20020516	WO 2001-AU1462	20011109
WO 2002038594	C2	20021107		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
AU 2002014810	A5	20020521	AU 2002-14810	20011109
US 2003103999	A1	20030605	US 2001-10160	20011109
BR 2001014835	A	20030701	BR 2001-14835	20011109
EP 1332154	A1	20030806	EP 2001-983297	20011109
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
PRIORITY APPLN. INFO.:	AU 2000-1381 A 20001110 US 2000-249596P P 20001117 WO 2001-AU1462 W 20011109			
AB	The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by Lawsonia intracellularis or similar or otherwise related microorganisms. In particular, the present invention provides a novel gene derived from Lawsonia intracellularis , which encodes an immunogenic polypeptide that is particularly useful as an antigen in a vaccine preparation for conferring humoral immunity against Lawsonia intracellularis and related pathogens in animal hosts, wherein said polypeptide is			

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selected from the group consisting of flhB, fliR, ntrC, glnH, motA, motB, tlyC, ytfM, and ytfN polypeptides, or a homolog, analog or derivative of any one or more of said polypeptides. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 2002:752377 HCAPLUS
DOCUMENT NUMBER: 137:277776
TITLE: Sequences of Mycoplasma hyopneumoniae antigen mhp3 and therapeutic and diagnosis uses
INVENTOR(S): King, Kendall Wayne; Madura, Rebecca Anne; Rosey, Everett Lee
PATENT ASSIGNEE(S): Pfizer Products Inc., USA
SOURCE: Eur. Pat. Appl., 38 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1245677	A1	20021002	EP 2001-303030	20010330
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
BR 2001002541	A	20020528	BR 2001-2541	20010329
JP 2002306169	A2	20021022	JP 2001-101364	20010330
PRIORITY APPLN. INFO.:			US 2000-676249	A 20000929
			EP 2001-303030	A 20010330

AB The present invention provides protein and DNA sequences of Mycoplasma hyopneumoniae antigen mhp3 gene. The present invention further relates to novel apoprotein antigens encoded by mhp3 gene for use in vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae. The invention further relates to methods, vector and host cells for recombinant production of such antigens. The invention also relates to diagnosis of infections in pig caused by Mycoplasma hyopneumoniae.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 5 OF 16 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-609319 [66] WPIDS
DOC. NO. CPI: C2002-172381
TITLE: Nucleic acids and proteins of gene MHP3 of Mycoplasma hyopneumoniae are used in vaccines for prophylaxis and treatment of infections caused by Mycoplasma hyopneumoniae.
DERWENT CLASS: B04 S03
INVENTOR(S): KING, K W; MADURA, R A; ROSEY, E L

Searcher : Shears 308-4994

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10/010160

PATENT ASSIGNEE(S): (PFIZ) PFIZER INC
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
BR 2001002541	A	20020528	(200266)*		1

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
BR 2001002541	A	BR 2001-2541	20010329

PRIORITY APPLN. INFO: US 2000-676249 20000929

AN 2002-609319 [66] WPIDS

AB BR 200102541 A UPAB: 20021014

NOVELTY - Nucleic acids and proteins of the gene MHP3 of Mycoplasma hyopneumoniae are used in vaccines for prophylaxis and treatment of infections caused by Mycoplasma hyopneumoniae.

USE - In the prevention and treatment of illnesses caused by infections by Mycoplasma hyopneumoniae.
Dwg.0/0

L21 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 3

ACCESSION NUMBER: 2001:261139 HCAPLUS

DOCUMENT NUMBER: 134:294510

TITLE: Sequences of Mycoplasma hyopneumoniae antigen mhp3 and therapeutic uses thereof

INVENTOR(S): King, Kendall Wayne; Madura, Rebecca
Anne; Rosey, Everett Lee .

PATENT ASSIGNEE(S): Pfizer Products Inc., USA

SOURCE: Eur. Pat. Appl., 38 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1090995	A2	20010411	EP 2000-308421	20000926
EP 1090995	A3	20010418		

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO

BR 2000004488	A	20011113	BR 2000-4488	20000927
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NZ 507205	A	20020301	NZ 2000-507205	20000928
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CN 1296953	A	20010530	CN 2000-129083	20000929
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JP 2001149085	A2	20010605	JP 2000-300778	20000929
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PRIORITY APPLN. INFO.: US 1999-156602P P 19990929

AB The present invention provides protein and DNA sequences of Mycoplasma hyopneumoniae antigen mhp3 gene. The present invention further relates to novel apoprotein antigens encoded by mhp3 gene for use in vaccines to prevent and treat diseases caused by infection with Mycoplasma hyopneumoniae. The invention further relates to method recombinant production of such antigens.

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L21 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:297553 HCAPLUS

DOCUMENT NUMBER: 134:321599

TITLE: Cloning of Lawsonia genes htrA, ponA, hypC, lysS, ycfW, abcl, and omp100, their encoded proteins or peptides and therapeutic use in diagnosis and as vaccine

INVENTOR(S): Rosey, Everett Lee

PATENT ASSIGNEE(S): Pfizer Products Inc., USA

SOURCE: Eur. Pat. Appl., 80 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1094070	A2	20010425	EP 2000-309125	20001017
EP 1094070	A3	20020109		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
US 6605696	B1	20030812	US 2000-689065	20001012
JP 2001169787	A2	20010626	JP 2000-320736	20001020
US 2003021802	A1	20030130	US 2002-210296	20020801
PRIORITY APPLN. INFO.:			US 1999-160922P	P 19991022
			US 1999-163868P	P 19991105
			US 2000-689065	A1 20001012

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in pigs or other animals caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism, such as porcine proliferative enteropathy (PPE). In particular, the present invention provides novel genes htrA, ponA, hypC, lysS, ycfW, abcl, and omp100 derived from **Lawsonia intracellularis** genomic regions A and B. These genes encode sequence homologs to lysyl-tRNA synthetase (gene lysS), transmembrane or integral membrane protein (abcl), hydrogenase maturation protein (hypC), penicillin binding protein (ponA), and periplasmic serine protease protein (htrA) resp. The invention also relates to constructing these gene expression vector to produce recombinant protein using E. coli. Methods of expressing recombinant htrA and omp100 proteins in E. coli are also provided. The invention also provides the immunogenic peptides or proteins encoded by these genes that are particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

L21 ANSWER 8 OF 16 WPIDS COPYRIGHT 2003 THOMSON DERWENT on STN

ACCESSION NUMBER: 2001-592540 [67] WPIDS

DOC. NO. NON-CPI: N2001-441503

DOC. NO. CPI: C2001-175788

TITLE: **Lawsonia intracellularis**

Searcher : Shears 308-4994

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10/010160

polynucleotide and encoded protein, used to prevent
Lawsonia intracellularis
infection.
DERWENT CLASS: B04 C06 D16 S03
INVENTOR(S): ROSEY, E L
PATENT ASSIGNEE(S): (PFIZ) PFIZER PROD INC
COUNTRY COUNT: 26
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
JP 2001169787	A	20010626	(200167)*		67
EP 1094070	A2	20010425	(200167)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
JP 2001169787	A	JP 2000-320736	20001020
EP 1094070	A2	EP 2000-309125	20001017

PRIORITY APPLN. INFO: US 1999-160922P 19991022

AN 2001-592540 [67] WPIDS

AB JP2001169787 A UPAB: 20011129

NOVELTY - An isolated polynucleotide molecule containing a nucleotide sequence encoding HtrA, PonA, HypC, LysS, YefW, ABC1 or Omp100 protein of **Lawsonia intracellularis**, or it's fragment or homolog, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) polynucleotide molecule containing more than 20 nucleotides having promotor activity and being found in nucleotides 2691-2890 of a 5445 nucleotide sequence, fully defined in the specification, or its complement;

(2) a recombinant vector containing the polynucleotide of (1);

(3) a transformed host cell transformed containing the novel vector;

(4) a polypeptide produced by the cell of (3);

(5) a gene construct containing a polynucleotide molecule which can be used for changing **Lawsonia** gene;

(6) a transformed cell containing the construct of (5);

(7) an isolated polypeptide produced by the cell of (6);

(8) an attenuated live vaccine containing the transformed cell of (6);

(9) a killed vaccine containing the cell of (6) in dead form; and

(10) an immunogenic composition containing an immunologically effective amount of the polypeptide of (3), and a carrier.

ACTIVITY - Antibacterial.

No biological data is given.

MECHANISM OF ACTION - Vaccine.

USE - The composition is useful for the prevention of **Lawsonia intracellularis** infection.

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L21 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2000:824297 HCAPLUS
DOCUMENT NUMBER: 134:1364
TITLE: Lawsonia-derived gene tlyA and related hemolysin
polypeptides, peptides and proteins and their
uses for diagnosis and treatment of avian and
porcine infections
INVENTOR(S): Panaccio, Michael; Rosey, Everett Lee;
Hasse, Detlef; Ankenbauer, Robert Gerard
PATENT ASSIGNEE(S): Pfizer Products Inc, USA; Agriculture Victoria
Services Pty Ltd; Pig Research and Development
Corporation
SOURCE: PCT Int. Appl., 86 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000069906	A1	20001123	WO 2000-AU439	20000511
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1177213	A1	20020206	EP 2000-924978	20000511
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
NZ 515363	A	20030725	NZ 2000-515363	20000511
PRIORITY APPLN. INFO.:			US 1999-134022P P	19990513
			WO 2000-AU439 W	20000511

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis** which encodes an immunogenic TylA hemolysin peptide, polypeptide or protein that is particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 2000:824295 HCAPLUS

Searcher : Shears 308-4994

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DOCUMENT NUMBER: 133:359825
TITLE: Lawsonia-derived gene flgE and related flagellar hook polypeptides, peptides and proteins and their uses for diagnosis and treatment of avian and porcine infections
INVENTOR(S): Panaccio, Michael; Rosey, Everett Lee; Sinistaj, Meri; Hasse, Detlef; Parsons, Jim; Ankenbauer, Robert Gerard
PATENT ASSIGNEE(S): Pfizer Products Inc., USA; Agriculture Victoria Services Pty Ltd; Pig Research and Development Corporation
SOURCE: PCT Int. Appl., 97 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000069904	A1	20001123	WO 2000-AU437	20000511
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
BR 2000011294	A	20020226	BR 2000-11294	20000511
EP 1181315	A1	20020227	EP 2000-924976	20000511
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
JP 2003516113	T2	20030513	JP 2000-618320	20000511
NZ 515331	A	20030725	NZ 2000-515331	20000511
US 2003157120	A1	20030821	US 2002-9823	20020813
PRIORITY APPLN. INFO.:			US 1999-133973P P	19990513
			WO 2000-AU437 W	20000511

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis** which encodes an immunogenic FlgE flagellar hook peptide, polypeptide or protein that is particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L21 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 6
ACCESSION NUMBER: 2000:824294 HCAPLUS
DOCUMENT NUMBER: 133:359824
TITLE: Lawsonia-derived gene sodC and related
superoxide dismutase polypeptides, peptides and
proteins and their uses for diagnosis and
treatment of avian and porcine infections
INVENTOR(S): Ankenbauer, Robert Gerard; Hasse, Detlef;
Panaccio, Michael; **Rosey, Everett Lee**;
Wright, Catherine
PATENT ASSIGNEE(S): Pfizer Products, Inc., USA; Pig Research and
Development Corp.; Agriculture Victoria Services
Pty., Ltd.
SOURCE: PCT Int. Appl., 85 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000069903	A1	20001123	WO 2000-AU436	20000511
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1177212	A1	20020206	EP 2000-924975	20000511
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
BR 2000011292	A	20020226	BR 2000-11292	20000511
JP 2003501013	T2	20030114	JP 2000-618319	20000511
PRIORITY APPLN. INFO.:			US 1999-133989P P	19990513
			WO 2000-AU436 W	20000511

AB The present invention relates generally to therapeutic compns. for the treatment and/or prophylaxis of intestinal disease conditions in animals and birds caused or exacerbated by **Lawsonia intracellularis** or similar or otherwise related microorganism. In particular, the present invention provides a novel gene derived from **Lawsonia intracellularis** which encodes an immunogenic SodC superoxide dismutase peptide, polypeptide or protein that is particularly useful as an antigen in vaccine preparation for conferring humoral immunity against **Lawsonia intracellularis** and related pathogens in animal hosts. The present invention is also directed to methods for the treatment and/or prophylaxis of such intestinal disease conditions and to diagnostic agents and procedures for detecting **Lawsonia intracellularis** or similar or otherwise related microorganisms.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L21 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 1998:558037 HCAPLUS
DOCUMENT NUMBER: 129:255827
TITLE: Identification and sequencing of the groE operon
and flanking genes of *Lawsonia*
intracellularis: use in phylogeny
AUTHOR(S): Dale, C. Jane H.; Moses, Eric K.; Ong,
Chin-Chui; Morrow, Chris J.; Reed, Michael B.;
Hasse, Dete; **Strugnell, Richard A.**
CORPORATE SOURCE: Victorian Institute of Animal Science, Victoria,
3049, Australia
SOURCE: Microbiology (Reading, United Kingdom) (1998),
144(8), 2073-2084
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Proliferative enteropathy (PE) is a complex of diseases of com.
importance to the pig industry. The obligate intracellular
bacterium *Lawsonia intracellularis* is
consistently associated with PE and pure cultures of this bacterium
have been used to reproduce PE in pigs. In this study *L.*
intracellularis bacteria were purified directly from
PE-affected tissue. DNA extracted from purified bacteria was used to
construct a partial genomic library which was screened using sera
from *L. intracellularis*-immunized rabbits. Two
seroreactive recombinant clones were identified, one of which
expressed proteins of 10 and 60 kDa. The sequence of the insert
from this clone, pISI-2, revealed ORFs with sequence similarity to
the groES/EL operon of *Escherichia coli*, the 50S ribosomal proteins
L21 and L27 of *E. coli*, a GTP-binding protein of *Bacillus subtilis*
and a possible protoporphyrinogen oxidase, HemK, of *E. coli*.
Primers designed from unique sequences from the pISI-2 insert
amplified DNA from infected, but not non-infected, porcine ilea; the
amplicon sequence obtained from tissue-cultured *L.*
intracellularis was identical to the corresponding sequence
in pISI-2, confirming the origin of the clone. The sequence of
L. intracellularis GroEL and other GroEL sequences
in the databases were used to construct a partial phylogenetic tree.
Anal. of the GroEL sequence relationship suggested that *L.*
intracellularis is not significantly related to other
organisms whose GroEL sequences are held in the databases and
supports previous data from 16S sequence analyses suggesting that
L. intracellularis is a member of a novel group of
enteric pathogens.
REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L21 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN DUPLICATE 8
ACCESSION NUMBER: 1997:171184 HCAPLUS
DOCUMENT NUMBER: 126:224028
TITLE: Characterization of the gene encoding Mhp1 from
Mycoplasma hyopneumoniae and examination of
Mhp1's vaccine potential
AUTHOR(S): King, Kendall W.; Faulds, Daryl H.;
Rosey, Everett L.; Yancey, Robert J.,
Jr.

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10/010160

CORPORATE SOURCE: Veterinary Infectious Disease, The Upjohn
Company, Kalamazoo, MI, 49001, USA
SOURCE: Vaccine (1997), 15(1), 25-35
CODEN: VACCDE; ISSN: 0264-410X
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The gene encoding Mhp1, a 124-kDa protein from Mycoplasma hyopneumoniae, has been cloned, sequenced, and its product characterized. No significant homol. to the gene or encoded polypeptide was found in the Genbank, NBRF, or PIR databases, though this protein appears similar to p97, a putative adhesin of M. hyopneumoniae. Two repeated motifs were identified within the 3' end of the gene and encoded polypeptide. The mhp1 gene was fused to the glutathione S-transferase (GST) gene from Schistosoma japonicum, enabling high-level expression and purification of the protein. Both the authentic and recombinant proteins were recognized by sera from pigs infected with M. hyopneumoniae. In an induced-disease model in pigs, coughing was reduced in animals vaccinated with recombinant GST-Mhp1, although differences were not significant. Only minimal protection against lung lesion formation was provided, and again differences between the Mhp1-vaccinated and nonvaccinated groups were not significant.

L21 ANSWER 14 OF 16 JAPIO (C) 2003 JPO on STN
ACCESSION NUMBER: 2002-306169 JAPIO
TITLE: NUCLEIC ACID OF MHP3 GENE OF MYCOPLASMA
HYOPNEUMONIAE, PROTEIN ENCODED BY THE GENE, AND
THEIR USES
INVENTOR: KING KENDALL WAYNE; MADURA REBECCA
ANNE; ROSEY EVERETT LEE
PATENT ASSIGNEE(S): PFIZER PROD INC
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 2002306169	A	20021022	Heisei	C12N015-09

APPLICATION INFORMATION

STN FORMAT: JP 2001-101364 20010330
ORIGINAL: JP2001101364 Heisei
PRIORITY APPLN. INFO.: JP 2001-101364 20010330
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 2002

AN 2002-306169 JAPIO

AB PROBLEM TO BE SOLVED: To provide a nucleic acid of mhp3 gene of Mycoplasma hyopneumoniae and a protein encoded by the gene.
SOLUTION: A new apoprotein encoded by mhp3 gene used in a vaccine for preventing and treating a disease caused by Mycoplasma hyopneumoniae and a method for producing the above antigen by the recombination, are provided.
COPYRIGHT: (C)2002, JPO

L21 ANSWER 15 OF 16 JAPIO (C) 2003 JPO on STN
ACCESSION NUMBER: 2001-169787 JAPIO
TITLE: LAWSONIA INTRACELLULARIS
PROTEIN, RELEVANT METHOD AND MATERIAL
INVENTOR: ROSEY EVERETT LEE

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PATENT ASSIGNEE(S): PFIZER PROD INC
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 2001169787	A	20010626	Heisei	C12N015-09

APPLICATION INFORMATION

STN FORMAT: JP 2000-320736 20001020
ORIGINAL: JP2000320736 Heisei
PRIORITY APPLN. INFO.: US 1999-160922 19991022
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 2001

AN 2001-169787 JAPIO

AB PROBLEM TO BE SOLVED: To isolate a **Lawsonia intracellularis** protein, and to provide a relevant method and a material.

SOLUTION: The isolated polypeptide molecule includes a nucleotide sequence encoding **L. intracellularis** htrA, ponA, hypC, lysS, ycfW, abcl or omp100 protein, a substantial part in the nucleotide sequence or its homologous sequence. Relevant polypeptides, immunogenic compositions and methods for assay are described.

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L21 ANSWER 16 OF 16 JAPIO (C) 2003 JPO on STN

ACCESSION NUMBER: 2001-149085 JAPIO

TITLE: NUCLEIC ACID OF mhp3 GENE OF Mycoplasma hyopneumoniae, PROTEIN ENCODED BY THE GENE, AND USES THEREOF

INVENTOR: KING KENDALL WAYNE; MADURA REBECCA ANNE; ROSEY EVERETT LEE

PATENT ASSIGNEE(S): PFIZER PROD INC

PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 2001149085	A	20010605	Heisei	C12N015-09

APPLICATION INFORMATION

STN FORMAT: JP 2000-300778 20000929
ORIGINAL: JP2000300778 Heisei
PRIORITY APPLN. INFO.: US 1999-156602 19990929
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined
Applications, Vol. 2001

AN 2001-149085 JAPIO

AB PROBLEM TO BE SOLVED: To obtain Mycoplasma hyopneumoniae mhp3 gene nucleic acid and a protein encoded by the nucleic acid.

SOLUTION: A new apoprotein antigen is provided which is encoded by mhp3 used in vaccine for preventing and treating a disease caused by the infection of Mycoplasma hyopneumoniae. A method for producing the antigen by the recombination is also provided.

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 05:12:07 ; Search time 2003 Seconds

(without alignments)
12703.838 Million cell updates/sec

Title: US-10-010-160-1

Perfect score: 622

Sequence: 1 atgtctgatgaccaccagtaa.....aattatgcagtcgcagatc 622

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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14: gb_vl:*
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28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	3.5	254	11 G04707	G04707 Human STS W
2	22	3.5	108534	2 HS12409	AL021327 Human STS W
3	22	3.5	127699	2 AC141496	AC141496 Ratnus no
4	22	3.5	136519	2 AL135926	AL135926 Human DNA
5	22	3.5	160961	2 AC141118	AC141118 Ratnus no
6	22	3.5	164604	2 BX296535	BX296535 Dantio rer
7	22	3.5	183901	2 AL356425	AL356425 Homo sapi
8	22	3.5	250935	2 AC135412	AC135412 Ratnus no
9	22	3.5	286790	2 AC096515	AC096515 Ratnus no
10	22	3.4	44284	2 AC013856	AC013856 Drosophila
11	21	3.4	60164	2 AC020373	AC020373 Drosophila
12	21	3.4	61913	2 AL671966	AL671966 Human DNA
13	21	3.4	82517	9 HS341D10	Z97985 Human DNA s
14	21	3.4	85518	3 AC005449	AC005449 Drosophila
15	21	3.4	127641	9 AL354827	AL354827 Human DNA
16	21	3.4	147078	2 AC080184	AC080184 Homo sapi
17	21	3.4	151802	2 AC114263	AC114263 Dictyoste
18	21	3.4	162556	9 AC006017	AC006017 Homo sapi
19	21	3.4	164018	10 AL646050	AL646050 Mouse DNA
20	21	3.4	166438	2 AC021838	AC021838 Homo sapi
21	21	3.4	168417	3 AC008187	AC008187 Drosophila
22	21	3.4	174595	2 AC114655	AC114655 Mus muscu
23	21	3.4	174712	10 AL831725	AL831725 Mouse DNA
24	21	3.4	174902	2 AC110071	AC110071 Homo sapi
25	21	3.4	191470	2 AC117760	AC117760 Mus muscu
26	21	3.4	193156	2 AC127272	AC127272 Mus muscu
27	21	3.4	193157	2 AC073853	AC073853 Homo sapi
28	21	3.4	194036	3 AC091388	AC091388 Drosophila
29	21	3.4	195342	9 AC009120	AC009120 Homo sapi
30	21	3.4	195514	2 AC109217	AC109217 Mus muscu
31	21	3.4	198088	9 AC078957	AC078957 Homo sapi
32	21	3.4	215435	2 AC126275	AC126275 Mus muscu
33	21	3.4	216734	5 AB073376	AB073376 Oryzias l
34	21	3.4	218708	2 AC021166	AC021166 Homo sapi
35	21	3.4	226584	2 AC145044	AC145044 Bos tauru
36	21	3.4	254050	3 PPA929358	PPA929358 Plasmodiu
37	21	3.4	256227	3 AE003827	AE003827 Drosophila
38	21	3.4	259474	3 HUAC004605	HUAC004605 Homo sapi
39	21	3.4	265215	3 AE003837	AE003837 Drosophila
40	20	3.2	172	3 DROMTMR2	J01409 Drosophila
41	20	3.2	191	3 DROMTMR2	J01410 Drosophila
42	20	3.2	237	3 DAU94254	U94254 Drosophila
43	20	3.2	237	3 DAU94257	U94257 Drosophila
44	20	3.2	237	3 DAU94259	U94259 Drosophila
45	20	3.2	237	3 DAU94261	U94261 Drosophila
46	20	3.2	237	3 DAU94264	U94264 Drosophila
47	20	3.2	237	3 DAU94265	U94265 Drosophila
48	20	3.2	256	3 DCU94255	U94255 Drosophila
49	20	3.2	256	3 DCU94256	U94256 Drosophila
50	20	3.2	256	3 DCU94258	U94258 Drosophila
51	20	3.2	256	3 DCU94260	U94260 Drosophila
52	20	3.2	256	3 DSU94263	U94263 Drosophila
53	20	3.2	256	3 SAU94262	U94262 Scaptomyza
54	20	3.2	593	3 AF246464	AF246464 Drosophila
55	20	3.2	604	3 DMU07291	U07291 Drosophila
56	20	3.2	604	3 DSU07288	U07288 Drosophila
57	20	3.2	606	3 DSU07294	U07294 Drosophila
58	20	3.2	606	3 DAU07298	U07298 Drosophila
59	20	3.2	607	3 DAU07284	U07284 Drosophila
60	20	3.2	607	3 DSU07310	U07310 Drosophila
61	20	3.2	608	3 DOU07302	U07302 Drosophila
62	20	3.2	610	3 DAU07274	U07274 Drosophila
63	20	3.2	610	3 DAU07280	U07280 Drosophila
64	20	3.2	610	3 DMU07318	U07318 Drosophila
65	20	3.2	610	3 DP007322	U07322 Drosophila

Pred. No. is the number of results predicted by chance to have a

C 66	20	3.2	610	3	DP007328	U07328 Drosophila	C 139	20	3.2	14916	3	AF200829	AF200829 Drosophila
C 67	20	3.2	610	3	DTU07306	U07306 Drosophila	C 140	20	3.2	14943	3	AF200846	AF200846 Drosophila
C 68	20	3.2	634	3	AF246504	AF246504 Drosophila	C 141	20	3.2	14943	3	AF200847	AF200847 Drosophila
C 69	20	3.2	642	3	AF246503	AF246503 Drosophila	C 142	20	3.2	14943	3	AF200848	AF200848 Drosophila
C 70	20	3.2	678	3	AF479797	AF479797 Drosophila	C 143	20	3.2	14943	3	AF200849	AF200849 Drosophila
C 71	20	3.2	680	3	AF246515	AF246515 Drosophila	C 144	20	3.2	14943	3	AF200850	AF200850 Drosophila
C 72	20	3.2	689	3	AF246496	AF246496 Drosophila	C 145	20	3.2	14943	3	AF200851	AF200851 Drosophila
C 73	20	3.2	689	3	AF246497	AF246497 Drosophila	C 146	20	3.2	14943	3	AF200852	AF200852 Drosophila
C 74	20	3.2	691	3	AF246500	AF246500 Drosophila	C 147	20	3.2	14943	3	AF200853	AF200853 Drosophila
C 75	20	3.2	691	3	AF246499	AF246499 Drosophila	C 148	20	3.2	14943	3	AF200854	AF200854 Drosophila
C 76	20	3.2	691	3	AF246501	AF246501 Drosophila	C 149	20	3.2	14943	3	AF200855	AF200855 Drosophila
C 77	20	3.2	691	3	AF246502	AF246502 Drosophila	C 150	20	3.2	14943	3	AF200856	AF200856 Drosophila
C 78	20	3.2	692	3	AF246493	AF246493 Drosophila	C 151	20	3.2	14943	3	AF200857	AF200857 Drosophila
C 79	20	3.2	692	3	AF246494	AF246494 Drosophila	C 152	20	3.2	14943	3	AF200858	AF200858 Drosophila
C 80	20	3.2	692	3	AF246505	AF246505 Drosophila	C 153	20	3.2	14946	3	AF200839	AF200839 Drosophila
C 81	20	3.2	692	3	AF246506	AF246506 Drosophila	C 154	20	3.2	14946	3	AF200840	AF200840 Drosophila
C 82	20	3.2	692	3	AF246507	AF246507 Drosophila	C 155	20	3.2	14946	3	AF200841	AF200841 Drosophila
C 83	20	3.2	692	3	AF246508	AF246508 Drosophila	C 156	20	3.2	14946	3	AF200842	AF200842 Drosophila
C 84	20	3.2	692	3	AF246509	AF246509 Drosophila	C 157	20	3.2	14946	3	AF200843	AF200843 Drosophila
C 85	20	3.2	692	3	AF246510	AF246510 Drosophila	C 158	20	3.2	14964	3	AF200832	AF200832 Drosophila
C 86	20	3.2	692	3	AF246512	AF246512 Drosophila	C 159	20	3.2	14966	3	AF200830	AF200830 Drosophila
C 87	20	3.2	692	3	AF246513	AF246513 Drosophila	C 160	20	3.2	14970	3	AF200838	AF200838 Drosophila
C 88	20	3.2	692	3	AF246516	AF246516 Drosophila	C 161	20	3.2	14972	3	AF200837	AF200837 Drosophila
C 89	20	3.2	692	3	AF246517	AF246517 Drosophila	C 162	20	3.2	14972	3	AF200833	AF200833 Drosophila
C 90	20	3.2	692	3	AF246518	AF246518 Drosophila	C 163	20	3.2	14973	3	AF200835	AF200835 Drosophila
C 91	20	3.2	693	3	AF246519	AF246519 Drosophila	C 164	20	3.2	14974	3	AF200836	AF200836 Drosophila
C 92	20	3.2	693	3	AF246495	AF246495 Drosophila	C 165	20	3.2	16019	3	MIDYRN	MIDYRN
C 93	20	3.2	694	3	AF246498	AF246498 Drosophila	C 166	20	3.2	21915	1	DMU37541	DMU37541
C 94	20	3.2	694	3	AF479810	AF479810 Paramecia	C 167	20	3.2	61823	2	AE000824	AE000824
C 95	20	3.2	695	3	AF246511	AF246511 Drosophila	C 168	20	3.2	73477	2	AC114647	AC114647
C 96	20	3.2	713	3	AF536639	AF536639 Cyprocepe	C 169	20	3.2	73477	2	AC108698	AC108698
C 97	20	3.2	713	3	AF536640	AF536640 Cyprocepe	C 170	20	3.2	74048	2	AC015895	AC015895 Homo sapi
C 98	20	3.2	716	3	AF479809	AF479809 Mycodros	C 171	20	3.2	82875	2	AC013482	AC013482
C 99	20	3.2	736	3	AF059892	AF059892 Drosophila	C 172	20	3.2	83408	8	AB078516	AB078516
C 100	20	3.2	741	3	AF479805	AF479805 Drosophila	C 173	20	3.2	89737	8	AC027036	AC027036
C 101	20	3.2	742	3	AF479811	AF479811 Samoa	C 174	20	3.2	93929	2	AC110967_3	AC110967_3
C 102	20	3.2	745	3	AF479807	AF479807 Drosophila	C 175	20	3.2	95581	8	AC015448	AC015448
C 103	20	3.2	746	3	AF479802	AF479802 Drosophila	C 176	20	3.2	96936	8	ATP8F6	ATP8F6
C 104	20	3.2	750	3	AF479808	AF479808 Drosophila	C 177	20	3.2	103479	9	AC004557	AC004557
C 105	20	3.2	761	3	MID116SR	X84412 D. lebanon	C 178	20	3.2	103479	9	AC140059	AC140059
C 106	20	3.2	761	3	MID116SR	X84411 D. lebanon	C 179	20	3.2	109003	9	AC006207	AC006207
C 107	20	3.2	761	3	ZAPMT16S	M93998 Zaprinus t	C 180	20	3.2	109290	9	AC108868	AC108868
C 108	20	3.2	785	3	DROMT16SA	M93995 Drosophila	C 181	20	3.2	110000	2	AC091359_2	AC091359_2
C 109	20	3.2	799	3	DROMT16SB	M93996 Drosophila	C 182	20	3.2	110000	2	AC109672	AC109672
C 110	20	3.2	905	3	DROMT16SV	M93989 Drosophila	C 183	20	3.2	111566	8	AC000348	AC000348
C 111	20	3.2	905	3	DROMT16SX	M93992 Drosophila	C 184	20	3.2	117072	9	AC010445	AC010445
C 112	20	3.2	905	3	DROMT16SY	M93993 Drosophila	C 185	20	3.2	126954	9	AL365440	AL365440
C 113	20	3.2	905	3	DROMT16SZ	M93994 Drosophila	C 186	20	3.2	127293	2	AC026917	AC026917
C 114	20	3.2	905	3	DROMT16T	M93988 Drosophila	C 187	20	3.2	141048	9	AC073621	AC073621
C 115	20	3.2	905	3	S45470	S45470 {fragment b	C 188	20	3.2	142690	2	AC102207	AC102207
C 116	20	3.2	905	3	S45471	S45471 {fragment b	C 189	20	3.2	145697	2	AC020642	AC020642
C 117	20	3.2	905	3	S45472	S45472 {fragment b	C 190	20	3.2	146437	2	AC020836	AC020836
C 118	20	3.2	905	3	S45475	S45475 {fragment b	C 191	20	3.2	147118	9	AC007513	AC007513
C 119	20	3.2	905	3	S45475	S45475 {fragment b	C 192	20	3.2	150214	2	AC011291	AC011291
C 120	20	3.2	1701	3	AF164579	AF164579 Drosophila	C 193	20	3.2	151252	2	AC024416	AC024416
C 121	20	3.2	1702	3	AF164578	AF164578 Drosophila	C 194	20	3.2	151948	2	AC024416	AC024416
C 122	20	3.2	1704	3	AF164594	AF164594 Drosophila	C 195	20	3.2	152080	2	AC024416	AC024416
C 123	20	3.2	1705	3	AF164588	AF164588 Drosophila	C 196	20	3.2	152080	2	AC024416	AC024416
C 124	20	3.2	1705	3	AF164589	AF164589 Drosophila	C 197	20	3.2	152080	2	AC024416	AC024416
C 125	20	3.2	1706	3	AF164587	AF164587 Drosophila	C 198	20	3.2	152080	2	AC024416	AC024416
C 126	20	3.2	1706	3	AF164586	AF164586 Drosophila	C 199	20	3.2	152080	2	AC024416	AC024416
C 127	20	3.2	1710	3	AF164581	AF164581 Drosophila	C 200	20	3.2	152080	2	AC024416	AC024416
C 128	20	3.2	1713	3	AF164591	AF164591 Drosophila	C 201	20	3.2	152080	2	AC024416	AC024416
C 129	20	3.2	1713	3	AF164592	AF164592 Drosophila	C 202	20	3.2	152080	2	AC024416	AC024416
C 130	20	3.2	1713	3	AF164593	AF164593 Drosophila	C 203	20	3.2	152080	2	AC024416	AC024416
C 131	20	3.2	1715	3	AF164585	AF164585 Drosophila	C 204	20	3.2	152080	2	AC024416	AC024416
C 132	20	3.2	1715	3	AF164586	AF164586 Drosophila	C 205	20	3.2	152080	2	AC024416	AC024416
C 133	20	3.2	1717	3	AF164583	AF164583 Drosophila	C 206	20	3.2	152080	2	AC024416	AC024416
C 134	20	3.2	1717	3	AF164584	AF164584 Drosophila	C 207	20	3.2	152080	2	AC024416	AC024416
C 135	20	3.2	1717	3	AF164585	AF164585 Drosophila	C 208	20	3.2	152080	2	AC024416	AC024416
C 136	20	3.2	1717	3	AF164586	AF164586 Drosophila	C 209	20	3.2	152080	2	AC024416	AC024416
C 137	20	3.2	1717	3	AF164587	AF164587 Drosophila	C 210	20	3.2	152080	2	AC024416	AC024416
C 138	20	3.2	1717	3	AF164588	AF164588 Drosophila	C 211	20	3.2	152080	2	AC024416	AC024416
C 139	20	3.2	1717	3	AF164589	AF164589 Drosophila	C 212	20	3.2	152080	2	AC024416	AC024416

C 212	20	3.2	172883	9	AP003967	Homo sapi	285	19	3.1	1109	3	PV1292977	AU292977 Plasmodiu
C 213	20	3.2	174098	9	AC005737	Homo sapi	286	19	3.1	1109	3	PV1297403	AU297403 Plasmodiu
C 214	20	3.2	174316	2	AC136975	Mus muscu	287	19	3.1	1113	3	AF164605	AF164605 Plasmodiu
C 215	20	3.2	176736	2	AC103853	Homo sapi	288	19	3.1	1156	3	PVU08977	PVU08977 Plasmodiu
C 216	20	3.2	180511	2	AC139523	Homo sapi	289	19	3.1	1161	3	PRAC51X	L05068 Plasmodiu
C 217	20	3.2	182375	2	AC105920	Homo sapi	290	19	3.1	1179	3	PV1278611	AU278611 Plasmodiu
C 218	20	3.2	184989	2	AC113392	Homo sapi	291	19	3.1	1179	3	PV1400910	PV1400910 Plasmodiu
C 219	20	3.2	185624	9	AC103923	Homo sapi	292	19	3.1	1375	3	PRAC5CA	M06070 Plasmodiu
C 220	20	3.2	187566	2	AC139029	Homo sapi	293	19	3.1	1561	11	AF383928	AF383928 Hevea bra
C 221	20	3.2	187727	2	AC064806	Homo sapi	294	19	3.1	1711	3	AF164582	AF164582 Drosophill
C 222	20	3.2	192296	2	AC102197	Mus muscu	295	19	3.1	1713	3	AF164580	AF164580 Drosophill
C 223	20	3.2	192626	2	AC119968	Mus muscu	296	19	3.1	1895	3	PRAC5A	M11926 Plasmodiu
C 224	20	3.2	193212	2	AP004370	Homo sapi	297	19	3.1	1908	6	108489	108489 Sequence 1
C 225	20	3.2	193390	2	AC013730	Homo sapi	298	19	3.1	2211	2	AC014697	AC014697 Drosophill
C 226	20	3.2	194431	2	AC120280	Homo sapi	299	19	3.1	4709	9	HSM803323	HSM803323 Plasmodiu
C 227	20	3.2	196436	2	BX511162	Danio rer	300	19	3.1	5849	1	PRU79731	PRU79731 Plasmodiu
C 228	20	3.2	199230	2	AC118531	Rattus no	301	19	3.1	10095	1	AE011536	AE011536 Leprosptir
C 229	20	3.2	200341	2	AC138403	Mus muscu	302	19	3.1	10432	1	AE0014994	AE0014994 Streptoco
C 230	20	3.2	203422	10	AL713863	Mus muscu	303	19	3.1	11162	1	AE006505	AE006505 Streptoco
C 231	20	3.2	203846	2	AC119431	Mus muscu	304	19	3.1	11165	1	AE009988	AE009988 Streptoco
C 232	20	3.2	209914	10	AL845291	Mouse DNA	305	19	3.1	15865	3	MITCCNNR	X65015 C-11thidia o
C 233	20	3.2	219248	2	AC132858	Mus muscu	306	19	3.1	20663	2	AC014972	AC014972 Drosophill
C 234	20	3.2	223606	2	AC013479	Homo sapi	307	19	3.1	33837	3	CEP27C8	Z68216 Caenorhabdi
C 235	20	3.2	224146	2	AC135482	Rattus no	308	19	3.1	33837	3	CEP27C8	Z68216 Caenorhabdi
C 236	20	3.2	225208	2	AC015561	Homo sapi	309	19	3.1	36411	9	AC016626	AC016626 Homo sapi
C 237	20	3.2	225639	9	AC108073	Homo sapi	310	19	3.1	36893	9	AC138034	AC138034 Homo sapi
C 238	20	3.2	230841	2	AC103437	Rattus no	311	19	3.1	37515	6	AX458481	AX458481 Sequence
C 239	20	3.2	232344	2	AC111782	Rattus no	312	19	3.1	37640	9	AC005605	AC005605 Homo sapi
C 240	20	3.2	232930	10	AC113761	Rattus no	313	19	3.1	38413	9	AC005601	AC005601 Homo sapi
C 241	20	3.2	240231	2	AC129735	Rattus no	314	19	3.1	38952	3	CEAC3	CEAC3 Caenorhabdi
C 242	20	3.2	241883	2	AC129610	Rattus no	315	19	3.1	41731	3	CBRG544F13	CBRG544F13 Caenorhab
C 243	20	3.2	242445	2	AC132613	Mus muscu	316	19	3.1	47738	2	AC125417	AC125417 Homo sapi
C 244	20	3.2	243005	2	AC134740	Homo sapi	317	19	3.1	48123	2	AC130288	AC130288 Homo sapi
C 245	20	3.2	243253	2	BX511211	Danio rer	318	19	3.1	50259	1	AE014142	AE014142 Streptoco
C 246	20	3.2	248367	2	AC094853	Rattus no	319	19	3.1	51984	2	AC018279	AC018279 Drosophill
C 247	20	3.2	251375	2	AC109422	Rattus no	320	19	3.1	55095	8	AC073506	AC073506 Arabidops
C 248	20	3.2	252460	2	AC132183	Rattus no	321	19	3.1	57166	9	AC009320	AC009320 Homo sapi
C 249	20	3.2	256014	2	AC098283	Rattus no	322	19	3.1	65361	2	AC091863	AC091863 Homo sapi
C 250	20	3.2	258045	2	AC126195	Rattus no	323	19	3.1	68399	9	AL592075	AL592075 Human DNA
C 251	20	3.2	259203	2	AC097682	Rattus no	324	19	3.1	69315	5	AL935277	AL935277 Zebrafish
C 252	20	3.2	260529	2	AC097076	Rattus no	325	19	3.1	72425	2	AC087684	AC087684 Homo sapi
C 253	20	3.2	261004	2	AC113198	Mus muscu	326	19	3.1	72425	2	AC087684	AC087684 Homo sapi
C 254	20	3.2	278964	2	AC115321	Rattus no	327	19	3.1	73947	9	AC068152	AC068152 Homo sapi
C 255	20	3.2	288068	2	AC131481	Rattus no	328	19	3.1	74998	9	AC009423	AC009423 Homo sapi
C 256	20	3.2	300000	9	AP002532	Homo sapi	329	19	3.1	85862	3	AC004433	AC004433 Drosophill
C 257	20	3.2	300830	2	AC096498	Rattus no	330	19	3.1	85902	2	AC127532	AC127532 Homo sapi
C 258	20	3.2	318620	2	AC110910	Mus muscu	331	19	3.1	86701	9	AL353654	AL353654 Human DNA
C 259	20	3.2	318620	2	AC110910	Mus muscu	332	19	3.1	86906	9	AC006926	AC006926 Homo sapi
C 260	20	3.2	319548	2	AC110863	Rattus no	333	19	3.1	92398	9	AL358432	AL358432 Human DNA
C 261	19	3.1	264	8	AY019354	Oryza sat	334	19	3.1	93418	9	AC008379	AC008379 Homo sapi
C 262	19	3.1	399	3	AF045723	Tritoma	335	19	3.1	94498	10	AL691453	AL691453 Mouse DNA
C 263	19	3.1	652	3	HSR330886	Homo sapi	336	19	3.1	96589	6	AX695845	AX695845 Sequence
C 264	19	3.1	672	3	AF479792	Amioloa pi	337	19	3.1	96976	5	AL928938	AL928938 Zebrafish
C 265	19	3.1	681	3	S73385	CSF=cltrums	338	19	3.1	98454	2	AL592068	AL592068 Homo sapi
C 266	19	3.1	781	8	AF412012	Grateloup	339	19	3.1	98533	2	AP003828	AP003828 Oryza sat
C 267	19	3.1	783	8	AF412013	Grateloup	340	19	3.1	100294	8	AP003828	AP003828 Oryza sat
C 268	19	3.1	989	6	AX035237	Sequence	341	19	3.1	100680	9	AC011461	AC011461 Homo sapi
C 269	19	3.1	989	6	AX342091	Sequence	342	19	3.1	101948	9	AC091955	AC091955 Homo sapi
C 270	19	3.1	989	6	AX342151	Sequence	343	19	3.1	110000	2	AC131645	AC131645 Homo sapi
C 271	19	3.1	990	6	AX441154	Sequence	344	19	3.1	110000	2	AC131645	AC131645 Homo sapi
C 272	19	3.1	990	6	AX441154	Sequence	345	19	3.1	110000	2	AC131645	AC131645 Homo sapi
C 273	19	3.1	996	3	AF240459	AF189471 Aclista s	346	19	3.1	110000	2	BR324231_1	BR324231_1 Continuation (2 of
C 274	19	3.1	1042	3	PVU08983	Plasmodiu	347	19	3.1	110000	9	AF491780_09	AF491780_09 Continuation (2 of
C 275	19	3.1	1060	3	AF436891	Plasmodiu	348	19	3.1	111791	10	AL646056	AL646056 Mouse DNA
C 276	19	3.1	1070	3	AF164604	Plasmodiu	349	19	3.1	112309	2	AC002290	AC002290 Homo sapi
C 277	19	3.1	1070	3	AF436890	Plasmodiu	350	19	3.1	112732	9	AL160007	AL160007 Human DNA
C 278	19	3.1	1071	3	AF164606	Plasmodiu	351	19	3.1	113109	9	HS475N16	HS475N16 Human DNA
C 279	19	3.1	1071	3	AF164607	Plasmodiu	352	19	3.1	115747	10	AC079439	AC079439 Mus muscu
C 280	19	3.1	1071	3	AF164608	Plasmodiu	353	19	3.1	119320	2	AC138180	AC138180 Homo sapi
C 281	19	3.1	1075	3	PVU08978	Plasmodiu	354	19	3.1	120000	9	AC004842	AC004842 Homo sapi
C 282	19	3.1	1075	3	PVU08979	Plasmodiu	355	19	3.1	120139	9	AC131281	AC131281 Homo sapi
C 283	19	3.1	1106	3	PV1295636	Plasmodiu	356	19	3.1	120516	10	AL929063	AL929063 Homo sapi
C 284	19	3.1	1107	3	PRAC5D	M34697 P.vivax cfr	357	19	3.1	121390	2	AC138985	AC138985 Homo sapi

C 358	19	3.1 121664	9	AC114498	AC114498 Homo sapi	431	19	3.1 171075	2	AC026842	AC026842 Homo sapi
C 359	19	3.1 122315	2	AL389917	AL389917 Homo sapi	432	19	3.1 171972	2	AC012388	AC012388 Drosophila
C 360	19	3.1 124120	2	AL157824	AL157824 Homo sapi	433	19	3.1 172539	2	BX247948	BX247948 Drosophila
C 361	19	3.1 124167	9	AP001874	AP001874 Homo sapi	434	19	3.1 172805	9	AL360270	AL360270 Homo sapi
C 362	19	3.1 125150	2	AC005450	AC005450 Drosophila	435	19	3.1 173074	2	AC009703	AC009703 Homo sapi
C 363	19	3.1 125623	3	AC115559	AC115559 Drosophila	436	19	3.1 173176	2	AC129175	AC129175 Mus muscu
C 364	19	3.1 127340	9	AC112907	AC112907 Homo sapi	437	19	3.1 173510	9	AC142333	AC142333 Pan trogl
C 365	19	3.1 132943	9	AL355003	AL355003 Homo sapi	438	19	3.1 173952	2	AC080087	AC080087 Homo sapi
C 366	19	3.1 133309	9	AL137843	AL137843 Homo sapi	439	19	3.1 174012	5	AL929503	AL929503 Zebrafish
C 367	19	3.1 133402	9	AL137843	AL137843 Homo sapi	440	19	3.1 174023	9	AC080089	AC080089 Homo sapi
C 368	19	3.1 135055	2	AC011873	AC011873 Homo sapi	441	19	3.1 174302	9	AC090710	AC090710 Homo sapi
C 369	19	3.1 138177	9	AL139266	AL139266 Homo sapi	442	19	3.1 174470	2	AC021888	AC021888 Homo sapi
C 370	19	3.1 138251	9	AC004908	AC004908 Homo sapi	443	19	3.1 174543	2	AC025190	AC025190 Homo sapi
C 371	19	3.1 141166	2	AC015578	AC015578 Homo sapi	444	19	3.1 174997	3	AC008256	AC008256 Drosophila
C 372	19	3.1 142157	2	AC102412	AC102412 Mus muscu	445	19	3.1 175612	2	AC102442	AC102442 Mus muscu
C 373	19	3.1 144848	2	AC140069	AC140069 Mus muscu	446	19	3.1 175651	10	AC124381	AC124381 Mus muscu
C 374	19	3.1 145055	3	AC007453	AC007453 Drosophila	447	19	3.1 176595	3	AC018483	AC018483 Drosophila
C 375	19	3.1 145327	9	AP004285	AP004285 Homo sapi	448	19	3.1 176982	5	AL732610	AL732610 Zebrafish
C 376	19	3.1 146585	8	CNS0808	AC097451 Homo sapi	449	19	3.1 177214	2	AC119972	AC119972 Mus muscu
C 377	19	3.1 146808	9	AC097451	AC097451 Homo sapi	450	19	3.1 177717	9	AC061958	AC061958 Homo sapi
C 378	19	3.1 148257	2	AC105992	AC105992 Mus muscu	451	19	3.1 177785	10	AC126936	AC126936 Mus muscu
C 379	19	3.1 148565	2	AC022052	AC022052 Homo sapi	452	19	3.1 177991	2	BX511030	BX511030 Drosophila
C 380	19	3.1 149988	2	AC011929	AC011929 Homo sapi	453	19	3.1 178501	2	AL392165	AL392165 Homo sapi
C 381	19	3.1 150109	2	AC144706	AC144706 Drosophila	454	19	3.1 179063	2	AC032027	AC032027 Homo sapi
C 382	19	3.1 150497	2	AC011860	AC011860 Homo sapi	455	19	3.1 179262	9	AL355343	AL355343 Homo sapi
C 383	19	3.1 150642	9	AP016309	AP016309 Homo sapi	456	19	3.1 180423	9	AC096575	AC096575 Homo sapi
C 384	19	3.1 151079	9	AP001596	AP001596 Homo sapi	457	19	3.1 180827	2	BX284110	BX284110 Drosophila
C 385	19	3.1 151846	2	AC102315	AC102315 Mus muscu	458	19	3.1 181240	2	AC140725	AC140725 Homo sapi
C 386	19	3.1 152055	2	AC118645	AC118645 Mus muscu	459	19	3.1 181266	2	AC016131	AC016131 Drosophila
C 387	19	3.1 152747	9	AC068050	AC068050 Homo sapi	460	19	3.1 181435	2	AC013387	AC013387 Homo sapi
C 388	19	3.1 152802	9	AC110274	AC110274 Homo sapi	461	19	3.1 182106	3	AC091499	AC091499 Homo sapi
C 389	19	3.1 153649	9	AL732372	AL732372 Homo sapi	462	19	3.1 182260	2	AC112922	AC112922 Mus muscu
C 390	19	3.1 153749	8	AP003019	AP003019 Homo sapi	463	19	3.1 183496	2	AC125075	AC125075 Mus muscu
C 391	19	3.1 154065	2	AC084079	AC084079 Homo sapi	464	19	3.1 183687	9	AC064864	AC064864 Homo sapi
C 392	19	3.1 154539	2	AC079187	AC079187 Homo sapi	465	19	3.1 183794	2	AC011877	AC011877 Homo sapi
C 393	19	3.1 154695	2	BX511160	BX511160 Drosophila	466	19	3.1 184040	2	AC013327	AC013327 Homo sapi
C 394	19	3.1 154848	9	AC016555	AC016555 Homo sapi	467	19	3.1 184778	2	AC023567	AC023567 Homo sapi
C 395	19	3.1 155612	2	AC127461	AC127461 Drosophila	468	19	3.1 185317	2	AL158983	AL158983 Homo sapi
C 396	19	3.1 156316	2	AC135688	AC135688 Homo sapi	469	19	3.1 185784	2	AC120860	AC120860 Mus muscu
C 397	19	3.1 156319	2	AB020863	AB020863 Mus muscu	470	19	3.1 186218	9	AP006248	AP006248 Homo sapi
C 398	19	3.1 156909	9	CNS05676	AL325982 Homo sapi	471	19	3.1 186457	2	AC068359	AC068359 Homo sapi
C 399	19	3.1 157058	2	AC018966	AC018966 Homo sapi	472	19	3.1 186462	2	AL391727	AL391727 Homo sapi
C 400	19	3.1 157292	2	AL603392	AL603392 Homo sapi	473	19	3.1 186935	2	AC022990	AC022990 Homo sapi
C 401	19	3.1 158024	9	AL136456	AL136456 Homo sapi	474	19	3.1 189354	5	AL844883	AL844883 Zebrafish
C 402	19	3.1 158745	9	AC093289	AC093289 Homo sapi	475	19	3.1 191028	8	PEU38804	PEU38804 Porphyra pu
C 403	19	3.1 159596	9	AC125266	AC125266 Mus muscu	476	19	3.1 191130	2	AC010897	AC010897 Homo sapi
C 404	19	3.1 160677	2	AP003127	AP003127 Homo sapi	477	19	3.1 191590	2	AL935124	AL935124 Mus muscu
C 405	19	3.1 161280	9	AC093903	AC093903 Homo sapi	478	19	3.1 191772	10	AC022825	AC022825 Homo sapi
C 406	19	3.1 162115	9	AC004896	AC004896 Homo sapi	479	19	3.1 192176	3	AL129219	AL129219 Mouse DNA
C 407	19	3.1 162115	3	AC008289	AC008289 Drosophila	480	19	3.1 192187	2	AC116920	AC116920 Drosophila
C 408	19	3.1 163012	3	AC008056	AC008056 Homo sapi	481	19	3.1 192404	9	CNS01DWO	AL132696 Human chr
C 409	19	3.1 163584	5	BX000453	BX000453 Zebrafish	482	19	3.1 192764	2	AC127099	AC127099 Rattus no
C 410	19	3.1 163585	5	AL929590	AL929590 Zebrafish	483	19	3.1 192927	9	AC142355	AC142355 Pan trogl
C 411	19	3.1 163666	5	AC007888	AC007888 Drosophila	484	19	3.1 193559	9	CNS01RPH4	AL160471 Human chr
C 412	19	3.1 164035	2	AC115018	AC115018 Homo sapi	485	19	3.1 194175	10	AC084071	AC084071 Mus muscu
C 413	19	3.1 164235	2	AC091925	AC091925 Homo sapi	486	19	3.1 194300	2	BX465217	BX465217 Drosophila
C 414	19	3.1 164668	2	AC012139	AC012139 Homo sapi	487	19	3.1 194508	9	AC096667	AC096667 Homo sapi
C 415	19	3.1 164748	2	AC127621	AC127621 Rattus no	488	19	3.1 195981	2	AC023948	AC023948 Homo sapi
C 416	19	3.1 164909	8	AP022186	AP022186 Cynididum	489	19	3.1 196282	2	AC144659	AC144659 Rattus no
C 417	19	3.1 164921	2	AC101994	AC101994 Mus muscu	490	19	3.1 196828	9	AC126088	AC126088 Rattus no
C 418	19	3.1 164972	2	AP004273	AP004273 Homo sapi	491	19	3.1 199487	2	AC069287	AC069287 Homo sapi
C 419	19	3.1 165038	8	HS436K10	HS436K10 Homo sapi	492	19	3.1 199866	3	AY003872	AY003872 Plasmid
C 420	19	3.1 165139	2	AC110195	AC110195 Mus muscu	493	19	3.1 201323	2	AC132747	AC132747 Rattus no
C 421	19	3.1 165358	2	AC101997	AC101997 Mus muscu	494	19	3.1 201418	2	AC121195	AC121195 Rattus no
C 422	19	3.1 166670	2	AC055861	AC055861 Homo sapi	495	19	3.1 202103	2	AC135379	AC135379 Rattus no
C 423	19	3.1 166928	2	AC009444	AC009444 Homo sapi	496	19	3.1 203634	9	CNS01DVL	AL155879 Human chr
C 424	19	3.1 167049	2	AP003370	AP003370 Homo sapi	497	19	3.1 203650	2	CNS01DVL	AL155879 Human chr
C 425	19	3.1 168594	9	AC016117	AC016117 Homo sapi	498	19	3.1 203650	2	CNS01DVL	AL155879 Human chr
C 426	19	3.1 168871	2	BX470069	BX470069 Drosophila	499	19	3.1 203650	2	CNS01DVL	AL155879 Human chr
C 427	19	3.1 168949	2	AC069164	AC069164 Homo sapi	500	19	3.1 203650	2	CNS01DVL	AL155879 Human chr
C 428	19	3.1 169903	2	BX469915	BX469915 Drosophila	501	19	3.1 203650	2	CNS01DVL	AL155879 Human chr
C 429	19	3.1 170370	2	AC120521	AC120521 Cantis fam	502	19	3.1 203650	2	CNS01DVL	AL155879 Human chr
C 430	19	3.1 171042	2	AC120521	AC120521 Cantis fam	503	19	3.1 203650	2	CNS01DVL	AL155879 Human chr

C 504	19	3.1 204068	2	AC103395	AC103395 Mus muscu	577	19	3.1 264752	10	AL669856	AL669856 Mouse DNA
C 505	19	3.1 204343	2	AL359496	AL359496 Homo sapi	C 578	19	3.1 266035	2	AC127791	AC127791 Rattus no
C 506	19	3.1 204520	10	AC129181	AC129181 Mus muscu	579	19	3.1 266391	2	AC097092	AC097092 Rattus no
C 507	19	3.1 205084	10	AC121859	AC121859 Mus muscu	580	19	3.1 266806	2	AC129387	AC129387 Rattus no
C 508	19	3.1 206893	2	AC115569	AC115569 Rattus no	581	19	3.1 267899	2	AC096980	AC096980 Rattus no
C 509	19	3.1 207129	2	AC102377	AC102377 Mus muscu	582	19	3.1 268213	2	AC103285	AC103285 Rattus no
C 510	19	3.1 207582	2	AC144674	AC144674 Rattus no	583	19	3.1 270068	2	AC113213	AC113213 Rattus no
C 511	19	3.1 208531	2	AC132353	AC132353 Mus muscu	C 584	19	3.1 275192	2	AC119208	AC119208 Rattus no
C 512	19	3.1 209280	2	AC131427	AC131427 Rattus no	585	19	3.1 280977	2	AC129751	AC129751 Rattus no
C 513	19	3.1 209521	9	AC021649	AC021649 Homo sapi	586	19	3.1 285045	2	AC116217	AC116217 Rattus no
C 514	19	3.1 210176	2	AC102529	AC102529 Mus muscu	C 587	19	3.1 294169	3	AE003821	AE003821 Drosophill
C 515	19	3.1 210385	2	AC009627	AC009627 Homo sapi	588	19	3.1 303808	3	AE003452	AE003452 Drosophill
C 516	19	3.1 210775	2	AL732518	AL732518 Mus muscu	589	19	3.1 309145	2	AC105907	AC105907 Mus muscu
C 517	19	3.1 211633	2	AC073609	AC073609 Mus muscu	C 590	19	3.1 312694	2	AC105837	AC105837 Rattus no
C 518	19	3.1 212416	2	BX005288	BX005288 Dantio rer	591	19	3.1 313050	3	PPA929352	PPA929352 Plasmodiu
C 519	19	3.1 213535	6	AX197417	AX197417 Sequence	C 592	19	3.1 325650	1	AP005145	AP005145 Streptoco
C 520	19	3.1 215535	6	AX223856	AX223856 Sequence	593	19	3.1 328990	1	AP005279	AP005279 Corynebact
C 521	19	3.1 216625	2	AC120950	AC120950 Rattus no	594	19	3.1 340000	9	AP001696	AP001696 Homo sapi
C 522	19	3.1 218179	2	AC122363	AC122363 Mus muscu	C 595	19	3.1 349751	3	PFMAL4P3	PFMAL4P3 Plasmodiu
C 523	19	3.1 218731	2	AC136554	AC136554 Rattus no	C 596	19	3.1 349960	6	AX282125	AX282125 Sequence
C 524	19	3.1 217015	3	AE003788	AE003788 Drosophill	C 597	19	3.1 349960	6	AX282717	AX282717 Sequence
C 525	19	3.1 217046	10	AC123389	AC123389 Mus muscu	598	19	3.1 349980	6	AX127148	AX127148 Sequence
C 526	19	3.1 217135	2	AC134535	AC134535 Mus muscu	599	19	3.1 349980	6	AX127149	AX127149 Sequence
C 527	19	3.1 218635	2	AC118338	AC118338 Rattus no	C 600	19	3.1 349980	6	AX344559	AX344559 Sequence
C 528	19	3.1 219711	2	AC127995	AC127995 Rattus no	C 601	19	3.1 349980	6	AX573240	AX573240 Sequence
C 529	19	3.1 219925	2	AC113968	AC113968 Mus muscu	C 602	18	2.9 339980	6	AR290578	AR290578 Sequence
C 530	19	3.1 220638	10	AL645723	AL645723 Mouse DNA	603	18	2.9 69	6	AD6071	AD6071 Sequence
C 531	19	3.1 223392	2	AC134359	AC134359 Rattus no	C 604	18	2.9 73	6	166509	166509 Sequence
C 532	19	3.1 223326	2	AC127905	AC127905 Rattus no	C 605	18	2.9 73	6	166518	166518 Sequence
C 533	19	3.1 224469	2	AC107245	AC107245 Rattus no	C 606	18	2.9 81	6	166524	166524 Sequence
C 534	19	3.1 226432	2	AC134654	AC134654 Rattus no	C 607	18	2.9 87	6	A26058	A26058 PI promoter
C 535	19	3.1 227550	2	AC102686	AC102686 Mus muscu	C 608	18	2.9 90	6	A26059	A26059 sPI promoter
C 536	19	3.1 228283	10	AF312994	AF312994 Mus muscu	C 609	18	2.9 90	6	166525	166525 Sequence
C 537	19	3.1 228326	2	AC103363	AC103363 Mus muscu	C 610	18	2.9 93	6	A26057	A26057 PI promoter
C 538	19	3.1 228989	2	AC136274	AC136274 Rattus no	C 611	18	2.9 93	6	166523	166523 Sequence
C 539	19	3.1 230754	2	BX004888	BX004888 Zebrafish	C 612	18	2.9 104	6	A09227	A09227 Synthetic n
C 540	19	3.1 233417	10	AL844146	AL844146 Mouse DNA	C 613	18	2.9 105	6	A09226	A09226 Synthetic n
C 541	19	3.1 234979	2	AC139651	AC139651 Rattus no	C 614	18	2.9 105	6	E01046	E01046 DNA sequenc
C 542	19	3.1 235426	2	AC121074	AC121074 Canis fam	C 615	18	2.9 108	6	A09229	A09229 Synthetic n
C 543	19	3.1 235553	2	AC020742	AC020742 Homo sapi	C 616	18	2.9 109	6	A09228	A09228 Synthetic n
C 544	19	3.1 236984	2	BX470098	BX470098 Dantio rer	C 617	18	2.9 142	6	A26063	A26063 annealed nu
C 545	19	3.1 237065	2	AC128999	AC128999 Rattus no	C 618	18	2.9 175	6	HSAA11975	HSAA11975 Homo sapi
C 546	19	3.1 237426	2	AC095707	AC095707 Rattus no	C 619	18	2.9 262	8	AF119070	AF119070 Homo sapi
C 547	19	3.1 237712	9	AC012634	AC012634 Homo sapi	C 620	18	2.9 307	10	MMDECORIN	MMDECORIN M.musculus
C 548	19	3.1 238158	2	AC139244	AC139244 Mus muscu	C 621	18	2.9 540	10	AF054142	AF054142 Rattus no
C 549	19	3.1 238818	2	AC103320	AC103320 Rattus no	C 622	18	2.9 555	14	VACCH9	VACCH9 Vaccinia vi
C 550	19	3.1 239246	2	AC112938	AC112938 Mus muscu	C 623	18	2.9 601	14	VACIKPA	VACIKPA Vaccinia vi
C 551	19	3.1 239464	2	AC103079	AC103079 Rattus no	C 624	18	2.9 615	9	HSAA12025	HSAA12025 Homo sapi
C 552	19	3.1 243767	2	AC111853	AC111853 Rattus no	C 625	18	2.9 617	11	G83731	G83731 S209P6039RB
C 553	19	3.1 241393	2	AC119105	AC119105 Rattus no	C 626	18	2.9 639	9	HSAA36341	HSAA36341 Homo sapi
C 554	19	3.1 241396	2	AC123333	AC123333 Rattus no	C 627	18	2.9 646	11	BV076336	BV076336 S212P6820
C 555	19	3.1 241725	2	AC109724	AC109724 Rattus no	C 628	18	2.9 650	1	AY075119	AY075119 Unculture
C 556	19	3.1 244598	2	AC106081	AC106081 Rattus no	C 629	18	2.9 687	3	AF332475	AF332475 Pulex sim
C 557	19	3.1 245273	2	AC137407	AC137407 Rattus no	C 630	18	2.9 687	3	AF332476	AF332476 Pulex sim
C 558	19	3.1 247037	2	AC094028	AC094028 Rattus no	C 631	18	2.9 711	3	AF536641	AF536641 Cryploceop
C 559	19	3.1 247730	2	AC112120	AC112120 Rattus no	C 632	18	2.9 805	9	AF179694	AF179694 Pongo pyg
C 560	19	3.1 248074	2	AC097404	AC097404 Rattus no	C 633	18	2.9 850	14	VACCH9	VACCH9 Vaccinia vac
C 561	19	3.1 249341	2	AC111667	AC111667 Rattus no	C 634	18	2.9 1029	10	AF483502	AF483502 Mus muscu
C 562	19	3.1 249984	2	AC094845	AC094845 Rattus no	C 635	18	2.9 1029	10	AF483503	AF483503 Mus muscu
C 563	19	3.1 252420	2	AB014841	AB014841 Plasmodiu	C 636	18	2.9 1041	9	AY190752	AY190752 Homo sapi
C 564	19	3.1 252902	2	AC129164	AC129164 Rattus no	C 637	18	2.9 1039	3	AY135360	AY135360 Plasmodiu
C 565	19	3.1 254007	2	AC094413	AC094413 Rattus no	C 638	18	2.9 1086	3	AF163868	AF163868 Eulachnus
C 566	19	3.1 254573	2	AC112554	AC112554 Rattus no	C 639	18	2.9 1113	3	AF164603	AF164603 Plasmodiu
C 567	19	3.1 254646	2	AC114850	AC114850 Rattus no	C 640	18	2.9 1123	8	AY168989	AY168989 Arabidops
C 568	19	3.1 255448	2	AC134596	AC134596 Mus muscu	C 641	18	2.9 1182	3	PFAPAPNEMG	PFAPAPNEMG Plasmodiu
C 569	19	3.1 257471	2	AC114371	AC114371 Rattus no	C 642	18	2.9 1182	3	PSU09765	PSU09765 Plasmodiu
C 570	19	3.1 257471	10	AL627213	AL627213 Mouse DNA	C 643	18	2.9 1182	3	PVU09738	PVU09738 Plasmodiu
C 571	19	3.1 259159	2	AC113333	AC113333 Rattus no	C 644	18	2.9 1189	1	AF311966	AF311966 Ehrlichia
C 572	19	3.1 260517	2	AC113318	AC113318 Rattus no	C 645	18	2.9 1212	3	PPACSB	PPACSB Plasmodiu
C 573	19	3.1 260880	2	AC134486	AC134486 Rattus no	C 646	18	2.9 1212	3	PPACSL	PPACSL Plasmodiu
C 574	19	3.1 262990	2	AC096412	AC096412 Rattus no	C 647	18	2.9 1272	3	PFACSC	PFACSC P. cynomolgi
C 575	19	3.1 263050	1	AP000981	AP000981 Sulfolobu	C 648	18	2.9 1281	3	PPACSG	PPACSG P. cynomolgi
C 576	19	3.1 263377	2	AC105647	AC105647 Rattus no	C 649	18	2.9 1311	10	RRDECRNMNR	RRDECRNMNR R. rattus mr

650	18	2.9	1335	3	PFACSM	M15102 P.cynomolg	723	18	2.9	16225	2	AC015354	AC015354 Drosophila
C 651	18	2.9	1372	10	MPFGIT	X53929 M.musculus	C 724	18	2.9	17538	6	AX346059	AX346059 Sequence
C 652	18	2.9	1448	9	AK025871	AK025871 Homo sapi	C 725	18	2.9	18047	9	HSDMDALU	Y13186 Homo sapien
C 653	18	2.9	1479	10	BC016419	BC016419 Mus muscu	C 726	18	2.9	18302	9	AL450266	AL450266 Human DNA
C 654	18	2.9	1547	10	RNDCN	X59859 R.norvegicu	C 727	18	2.9	19295	2	AC112177	AC112177 Homo sapi
C 655	18	2.9	1605	10	MUSMEL18	D90085 Mus muscucu	C 728	18	2.9	19459	6	AX344208	AX344208 Homo sapi
C 656	18	2.9	1708	3	AF164595	AF164595 Drosophila	C 729	18	2.9	19459	6	AX348959	AX348959 Sequence
C 657	18	2.9	2000	6	AX595024	AX595024 Sequence	C 730	18	2.9	21509	3	DMC25D2	DMC25D2
C 658	18	2.9	2242	6	I08490	I08490 Sequence 3	C 731	18	2.9	24643	8	SPAC6C3	SPAC6C3
C 660	18	2.9	2755	9	HSMB03480	AK074333 Homo sapi	C 732	18	2.9	25138	8	HSTERR2	AF128894 Homo sapi
C 661	18	2.9	2884	10	BC031204	BC031204 Mus muscu	C 733	18	2.9	25407	8	AP006359	AP006359
C 662	18	2.9	2890	9	BC041560	BC041560 Homo sapi	C 734	18	2.9	26522	3	U29537	U29537
C 663	18	2.9	2942	9	AK094680	AK094680 Homo sapi	C 735	18	2.9	27991	3	CER44N6	CER44N6
C 664	18	2.9	3014	9	HSU57317	U57317 Homo sapien	C 736	18	2.9	29678	3	HSDMDINT	HSDMDINT
C 665	18	2.9	3142	6	AX704744	AX704744 Sequence	C 737	18	2.9	32784	3	CEP0865	CEP0865
C 666	18	2.9	3179	6	AX003139	AX003139 Sequence	C 738	18	2.9	33380	2	AC139172	AC139172
C 667	18	2.9	3181	6	AX338107	AX338107 Sequence	C 739	18	2.9	33995	2	CEK11B4	CEK11B4
C 668	18	2.9	3234	8	NTA131837	AJ131837 Nicotiana	C 740	18	2.9	35641	2	AC014835	AC014835
C 669	18	2.9	3577	8	SCYBR245C	Z36114 S.cerevisia	C 741	18	2.9	36885	3	AC024881	AC024881
C 670	18	2.9	3846	1	AY251553	AY251553 Clostridi	C 742	18	2.9	37770	3	AL355590	AL355590
C 671	18	2.9	4043	1	CLOBN	D49440 Clostridiu	C 743	18	2.9	39337	3	U39848	U39848
C 672	18	2.9	4231	6	AX210645	AX210645 Sequence	C 744	18	2.9	39488	2	DMC56F3	DMC56F3
C 673	18	2.9	4231	6	AX686744	AX686744 Sequence	C 745	18	2.9	39526	2	AC003961	AC003961
C 674	18	2.9	4231	6	AF071202	AF071202 Homo sapi	C 746	18	2.9	39526	2	AP001058	AP001058
C 675	18	2.9	4262	9	BC027907	BC027907 Homo sapi	C 747	18	2.9	41051	9	AC144442	AC144442
C 676	18	2.9	4412	9	AF169693	AF169693 Homo sapi	C 748	18	2.9	41598	9	HS16M16	HS16M16
C 677	18	2.9	4479	7	CBCPHGX1	X53751 Clostridiu	C 749	18	2.9	43129	2	AC131379	AC131379
C 678	18	2.9	4592	7	CSTC1T0X	D90210 Bacterioph	C 750	18	2.9	43553	2	AL357372	AL357372 Human DNA
C 679	18	2.9	4638	10	BC032273	BC032273 Mus muscu	C 751	18	2.9	43593	9	AC003960	AC003960 Human Cos
C 680	18	2.9	4712	1	CBBPNC1M	X71126 C.botulinu	C 752	18	2.9	43982	8	AC007289	AC007289
C 681	18	2.9	5127	6	AX344666	AX344666 Sequence	C 753	18	2.9	44227	8	AF275271	AF275271
C 682	18	2.9	5333	6	AX598849	AX598849 Sequence	C 754	18	2.9	45211	3	U29381	U29381
C 683	18	2.9	5333	6	AX598995	AX598995 Sequence	C 755	18	2.9	45820	2	AC014581	AC014581
C 684	18	2.9	5654	10	AK122303	AK122303 Mus muscu	C 756	18	2.9	46843	8	SPBC530	SPBC530
C 685	18	2.9	5876	10	MMU536155	AJ536155 Mus muscu	C 757	18	2.9	50000	6	AR211703	AR211703
C 686	18	2.9	6082	6	AR261061	AR261061 Sequence	C 758	18	2.9	50308	2	AC099858	AC099858 Mus muscu
C 687	18	2.9	6082	6	AR278592	AR278592 Sequence	C 759	18	2.9	50960	2	AC017313	AC017313
C 688	18	2.9	6082	6	AX141045	AX141045 Sequence	C 760	18	2.9	51552	6	AR266023	AR266023
C 689	18	2.9	6082	6	AX200905	AX200905 Sequence	C 761	18	2.9	51757	2	AC007025	AC007025
C 690	18	2.9	6082	6	AX267561	AX267561 Sequence	C 762	18	2.9	53570	2	AC100955	AC100955
C 691	18	2.9	6377	9	HSMB05107	AL833830 Homo sapi	C 763	18	2.9	53932	2	AP0023371	AP0023371
C 692	18	2.9	6533	14	AF189155	AF189155 Hantaviru	C 764	18	2.9	54472	8	AP004542	AP004542 Lotus jap
C 693	18	2.9	6550	14	PVLSOTKMO	Z65548 Puumala vir	C 765	18	2.9	54589	2	AL014460	AL014460 Drosophila
C 694	18	2.9	6710	6	AX008265	AX008265 Sequence	C 766	18	2.9	54727	9	AL357336	AL357336 Human DNA
C 695	18	2.9	7218	6	I66494	I66494 Sequence 14	C 767	18	2.9	55161	2	AC130684	AC130684 Homo sapi
C 696	18	2.9	7285	8	AF309806	AF309806 Populus b	C 768	18	2.9	56531	2	AC105232	AC105232
C 697	18	2.9	7379	2	HSMB03374	AL832067 Homo sapi	C 769	18	2.9	56891	2	AC101012	AC101012 Mus muscu
C 698	18	2.9	7795	2	AC066600	AC066600 Homo sapi	C 770	18	2.9	57049	9	HSDB58A12	HSDB58A12
C 699	18	2.9	7827	2	AC017447	AC017447 Drosophila	C 771	18	2.9	57893	2	AC095868-3	AC095868-3
C 700	18	2.9	8313	6	I66482	I66482 Sequence 2	C 772	18	2.9	58006	2	AC005127	AC005127
C 701	18	2.9	8333	6	AX277950	AX277950 Sequence	C 773	18	2.9	58333	2	AC020257	AC020257
C 702	18	2.9	8333	6	AX323641	AX323641 Sequence	C 774	18	2.9	58460	9	AL512299	AL512299
C 703	18	2.9	8333	6	AX346404	AX346404 Sequence	C 775	18	2.9	58473	9	AL449103	AL449103
C 704	18	2.9	8710	6	I60241	I60241 Sequence 3	C 776	18	2.9	58484	9	AL137122	AL137122
C 705	18	2.9	9019	6	I60242	I60242 Sequence 4	C 777	18	2.9	59250	2	AC144344	AC144344 Medicago
C 706	18	2.9	9064	8	MTK417911	I60242 Sequence 3	C 778	18	2.9	59272	2	AL592490	AL592490 Human DNA
C 707	18	2.9	9454	6	I66483	I66483 Sequence 3	C 779	18	2.9	60391	3	AC024796	AC024796 Caenorhab
C 708	18	2.9	9613	1	CBCCTOX	X63389 Botulinum b	C 780	18	2.9	60740	2	AC016557	AC016557
C 709	18	2.9	9613	1	CBCCTOX	X63389 Botulinum b	C 781	18	2.9	60778	2	AC092921-4	AC092921-4
C 710	18	2.9	9689	1	CBP1CWTCL	X64433 Clostridiu	C 782	18	2.9	61392	2	AC137565	AC137565
C 711	18	2.9	9917	6	I66496	I66496 Sequence 16	C 783	18	2.9	61920	2	AC021270	AC021270 Homo sapi
C 712	18	2.9	10605	1	AE015601	AE015601 Shewanella	C 784	18	2.9	62909	6	AX067457	AX067457
C 713	18	2.9	10781	9	HSU58767	U58767 Homo sapien	C 785	18	2.9	63571	3	AC005126	AC005126
C 714	18	2.9	11505	1	AE011693	AE011693 Xanthomon	C 786	18	2.9	63931	2	AC120211	AC120211
C 715	18	2.9	11614	1	AB031766	AB031766 Clostridi	C 787	18	2.9	64580	2	AC106282-4	AC106282-4
C 716	18	2.9	11747	1	AB061780	AB061780 Clostridi	C 788	18	2.9	64840	2	AC129551	AC129551 Mus muscu
C 717	18	2.9	12297	7	CBCBONT	X72793 Clostridiu	C 789	18	2.9	66118	9	AC109479	AC109479 Homo sapi
C 718	18	2.9	12379	1	AE012980	AE012980 Thermococ	C 790	18	2.9	68790	9	HSJ287H17	HSJ287H17
C 719	18	2.9	13326	14	VACLIVPF	MS7977 Vaccinia vi	C 791	18	2.9	68870	9	AC130292	AC130292
C 720	18	2.9	14867	3	AE001398	AE001398 Plasmodiu	C 792	18	2.9	68870	9	HS92M18	HS92M18
C 721	18	2.9	16200	6	AX405492	AX405492 Sequence	C 793	18	2.9	68903	9	AC087718	AC087718
C 722	18	2.9	16200	6	AX405493	AX405493 Sequence	C 795	18	2.9	70329	2	AC087718	AC087718

C 796	18	2.9	71371	9	AL356357	AL356357 Human DNA	C 869	18	2.9	106441	9	HSJ803J11	AL117350 Human DNA
C 797	18	2.9	72854	2	AC019316	AC019316 Homo sapi	870	18	2.9	107139	2	AL360223	AL360223 Homo sapi
C 798	18	2.9	72853	2	AC023432	AC023432 Homo sapi	C 871	18	2.9	107403	2	AL141864	AC141864 Homo sapi
799	18	2.9	73371	9	AC004872	AC004872 Homo sapi	C 872	18	2.9	107963	2	AC144517	AC144517 Homo sapi
800	18	2.9	73811	9	AL355879	AL355879 Human DNA	C 873	18	2.9	108718	2	AC008837	AC008837 Homo sapi
C 801	18	2.9	73811	9	AC091817	AC091817 Homo sapi	C 874	18	2.9	109224	2	AL356434	AL356434 Homo sapi
C 802	18	2.9	74237	9	AC098809	AC098809 Papio anu	C 875	18	2.9	109359	9	AC004857	AC004857 Homo sapi
C 803	18	2.9	74729	9	HS703H14	HS703H14 Homo sapi	C 876	18	2.9	109745	9	AC025469	AC025469 Homo sapi
C 804	18	2.9	75153	2	AC134293	AC134293 Rattus no	C 877	18	2.9	109891	9	AL353897	AL353897 Homo sapi
C 805	18	2.9	75276	9	AC008861	AC008861 Homo sapi	C 878	18	2.9	110000	2	AC079625	AC079625 Homo sapi
C 806	18	2.9	75359	9	AL359013	AL359013 Human DNA	C 879	18	2.9	110000	2	AC079845	AC079845 Homo sapi
C 807	18	2.9	76095	2	AC012753	AC012753 Drosophila	C 880	18	2.9	110000	2	AC096395	AC096395 Rattus no
C 808	18	2.9	76828	2	AC032029	AC032029 Homo sapi	C 881	18	2.9	110000	2	AC117030	AC117030 Homo sapi
C 809	18	2.9	77331	9	AL354983	AL354983 Human DNA	C 882	18	2.9	110000	2	AC118144	AC118144 Homo sapi
C 810	18	2.9	78467	9	AC008078	AC008078 Homo sapi	C 883	18	2.9	110000	2	AC119122	AC119122 Rattus no
C 811	18	2.9	79418	2	AC005429	AC005429 Drosophila	C 884	18	2.9	110000	2	AC119122	AC119122 Rattus no
C 812	18	2.9	79418	2	AC128461	Continuation (5 of	C 885	18	2.9	110000	2	AC128461	Continuation (5 of
C 813	18	2.9	79506	9	AL137247	AL137247 Human DNA	C 886	18	2.9	110000	2	AC128461	Continuation (5 of
C 814	18	2.9	81000	9	AB038161	AB038161 Homo sapi	C 887	18	2.9	110000	2	AC127805	AC127805 Homo sapi
C 815	18	2.9	81414	8	AB024037	AB024037 Arabidops	C 888	18	2.9	110000	2	AC128296	AC128296 Homo sapi
C 816	18	2.9	82483	9	AL391058	AL391058 Human DNA	C 889	18	2.9	110000	2	AL731895	AL731895 Homo sapi
C 817	18	2.9	83079	9	AC004538	AC004538 Homo sapi	C 890	18	2.9	110000	2	BM324111	BM324111 Homo sapi
C 818	18	2.9	83382	9	AL390793	AL390793 Human DNA	C 891	18	2.9	110000	2	PFMAL13	PFMAL13 Homo sapi
C 819	18	2.9	85638	9	AC108126	AC108126 Homo sapi	C 892	18	2.9	110000	2	PFMAL6P1	PFMAL6P1 Homo sapi
C 820	18	2.9	86162	2	AC126786	AC126786 Medicago	C 893	18	2.9	110000	2	BD061520	BD061520 Homo sapi
C 821	18	2.9	88512	8	FL1H2	FL1H2 Arabidops	C 894	18	2.9	110000	6	AC145127	AC145127 Homo sapi
C 822	18	2.9	88557	2	AL136314	AL136314 Human DNA	C 895	18	2.9	110000	8	AF438327	AF438327 Homo sapi
C 823	18	2.9	88735	2	AF165178	AF165178 Homo sapi	C 896	18	2.9	110000	8	AF058825	AF058825 Arabidops
C 824	18	2.9	90140	2	AC021612	AC021612 Homo sapi	C 897	18	2.9	110157	2	AC141111	AC141111 Homo sapi
C 825	18	2.9	90140	2	AC021612	AC021612 Homo sapi	C 898	18	2.9	110575	2	AP004969	AP004969 Lotus jap
C 826	18	2.9	90441	2	AC123574	AC123574 Medicago	C 899	18	2.9	110752	8	AL354766	AL354766 Human DNA
C 827	18	2.9	90461	2	AC118467	Continuation (5 of	C 900	18	2.9	111170	9	HSJ617C6	HSJ617C6 Homo sapi
C 828	18	2.9	90604	9	AC006525	AC006525 Homo sapi	C 901	18	2.9	111491	8	ATF1C18	ATF1C18 Homo sapi
C 829	18	2.9	90737	9	AB001351	AB001351 Homo sapi	C 902	18	2.9	111517	9	ATF1C18	ATF1C18 Homo sapi
C 830	18	2.9	91172	9	AL356601	AL356601 Human DNA	C 903	18	2.9	112672	9	AC010455	AC010455 Homo sapi
C 831	18	2.9	91228	8	ATF14M19	ATF14M19 Arabidops	C 904	18	2.9	112846	2	AP000718	AP000718 Homo sapi
C 832	18	2.9	91469	9	AL356963	AL356963 Human DNA	C 905	18	2.9	112884	2	AL596268	AL596268 Human DNA
C 833	18	2.9	91987	9	AC125362	AC125362 Homo sapi	C 906	18	2.9	113335	9	AL596268	AL596268 Human DNA
C 834	18	2.9	92376	8	AC006282	AC006282 Arabidops	C 907	18	2.9	113729	9	AF266011	AF266011 Homo sapi
C 835	18	2.9	92493	8	ATF23J17	ATF23J17 Arabidops	C 908	18	2.9	113826	9	AL133378	AL133378 Human DNA
C 836	18	2.9	92564	9	ATY007685	ATY007685 Homo sapi	C 909	18	2.9	114022	9	AL157952	AL157952 Human DNA
C 837	18	2.9	92883	2	AC142027	AC142027 Rattus no	C 910	18	2.9	115304	9	AL138775	AL138775 Human DNA
C 838	18	2.9	93609	2	AL357673	AL357673 Homo sapi	C 911	18	2.9	115767	2	AC012310	AC012310 Homo sapi
C 839	18	2.9	93717	9	AL357673	AL357673 Homo sapi	C 912	18	2.9	116476	2	AC127167	AC127167 Medicago
C 840	18	2.9	94516	9	AC112126	AC112126 Homo sapi	C 913	18	2.9	116513	9	HS48737	HS48737 Homo sapi
C 841	18	2.9	94730	9	AB000030	AB000030 Homo sapi	C 914	18	2.9	116629	2	AC11485	AC11485 Homo sapi
C 842	18	2.9	95347	9	HSJ081L22	HSJ081L22 Human DNA	C 915	18	2.9	116795	9	AC015060	AC015060 Homo sapi
C 843	18	2.9	96203	9	AL135788	AL135788 Human DNA	C 916	18	2.9	117723	8	AC023279	AC023279 Homo sapi
C 844	18	2.9	96203	8	ATF10N7	ATF10N7 Arabidops	C 917	18	2.9	117723	9	AC116365	AC116365 Homo sapi
C 845	18	2.9	96843	9	AC009496	AC009496 Homo sapi	C 918	18	2.9	117755	9	AC092686	AC092686 Homo sapi
C 846	18	2.9	97653	2	AC137570	AC137570 Homo sapi	C 919	18	2.9	117951	9	AL359821	AL359821 Human DNA
C 847	18	2.9	97736	9	AC0093845	AC0093845 Homo sapi	C 920	18	2.9	117954	9	AC002065	AC002065 Homo sapi
C 848	18	2.9	97818	2	AC011259	AC011259 Homo sapi	C 921	18	2.9	118335	8	AC006193	AC006193 Arabidops
C 849	18	2.9	98391	2	AC106733	AC106733 Homo sapi	C 922	18	2.9	118453	2	AC135796	AC135796 Homo sapi
C 850	18	2.9	98613	2	AC013426	AC013426 Homo sapi	C 923	18	2.9	118933	2	AC020205	AC020205 Drosophila
C 851	18	2.9	99369	9	AC112140	AC112140 Homo sapi	C 924	18	2.9	118995	9	AC005368	AC005368 Homo sapi
C 852	18	2.9	99630	2	AC142060	AC142060 Rattus no	C 925	18	2.9	120638	2	AC122168	AC122168 Homo sapi
C 853	18	2.9	100000	2	AB0000144	AB0000144 Homo sapi	C 926	18	2.9	120962	2	AC141114	AC141114 Medicago
C 854	18	2.9	101244	2	AC121334	AC121334 Medicago	C 927	18	2.9	120985	2	AC099651	AC099651 Homo sapi
C 855	18	2.9	101363	2	AC129090	AC129090 Medicago	C 928	18	2.9	121129	9	AL357315	AL357315 Human DNA
C 856	18	2.9	101611	9	AC018706	AC018706 Homo sapi	C 929	18	2.9	122049	9	HSB16C10	HSB16C10 Homo sapi
C 857	18	2.9	103487	9	AL449343	AL449343 Human DNA	C 930	18	2.9	122107	2	AC144482	AC144482 Medicago
C 858	18	2.9	104008	2	AC140022	AC140022 Medicago	C 931	18	2.9	122135	2	AC137552	AC137552 Medicago
C 859	18	2.9	104339	2	AF235105	AF235105 Homo sapi	C 932	18	2.9	122665	2	BM004777	BM004777 Dario rer
C 860	18	2.9	104573	2	AC144618	AC144618 Medicago	C 933	18	2.9	122986	2	AC004915	AC004915 Homo sapi
C 861	18	2.9	104687	2	AC144724	AC144724 Medicago	C 934	18	2.9	123147	2	AC140029	AC140029 Homo sapi
C 862	18	2.9	104738	8	ATF20B18	ATF20B18 Arabidops	C 935	18	2.9	123631	9	HS22F01	HS22F01 Homo sapi
C 863	18	2.9	104846	9	HSB54J116	HSB54J116 Human DNA	C 936	18	2.9	123829	10	AC113263	AC113263 Mus muscu
C 864	18	2.9	105335	9	AL5107374	AL5107374 Homo sapi	C 937	18	2.9	125170	9	AC133796	AC133796 Homo sapi
C 865	18	2.9	105515	2	AL512786	AL512786 Homo sapi	C 938	18	2.9	125357	2	AC136974	AC136974 Homo sapi
C 866	18	2.9	105657	2	AL365503	AL365503 Human DNA	C 939	18	2.9	125403	9	AC008929	AC008929 Homo sapi
C 867	18	2.9	105857	2	AC140028	AC140028 Medicago	C 940	18	2.9	125720	2	AC136138	AC136138 Homo sapi
C 868	18	2.9	106180	2	AC144728	AC144728 Medicago	C 941	18	2.9	125992	2	AC142222	AC142222 Medicago

```
942 18 2.9 126469 9 AC090022 Homo sapi
943 18 2.9 126501 9 HS708F5
944 18 2.9 127757 9 AC004468 Human DNA
945 18 2.9 128243 9 AC104707 Oryza sat
946 18 2.9 128366 9 AC1356782 Human DNA
947 18 2.9 128595 2 AL136179 Human DNA
948 18 2.9 128728 8 AC126794 Human DNA
949 18 2.9 129512 8 AC126794 Human DNA
950 18 2.9 130412 2 AL513221
951 18 2.9 131266 10 AL669868
952 18 2.9 131490 10 AC122207
953 18 2.9 132254 3 AC116330
954 18 2.9 132493 8 AC126785 Medicago
955 18 2.9 132702 8 AC126785 Medicago
956 18 2.9 133085 2 AC073510
957 18 2.9 133226 2 AL512364
958 18 2.9 133304 9 AC107079 Homo sapi
959 18 2.9 133847 9 AC096666 Homo sapi
960 18 2.9 134105 2 AC073383 Homo sapi
961 18 2.9 134350 2 AC140027
962 18 2.9 134513 10 AL444151
963 18 2.9 134601 2 AP004803
964 18 2.9 134628 9 AC090440
965 18 2.9 134780 9 HS45F6
966 18 2.9 134841 9 AC016689 Human DNA
967 18 2.9 135089 2 BX511186
968 18 2.9 135298 2 AC084873 Homo sapi
969 18 2.9 135521 9 AC005858 Homo sapi
970 18 2.9 135953 9 AL583854 Human DNA
971 18 2.9 137125 2 AC116724
972 18 2.9 137260 2 BX511307
973 18 2.9 137863 2 AC144592
974 18 2.9 137995 2 AC025009 Homo sapi
975 18 2.9 138388 9 AC055854 Homo sapi
976 18 2.9 138419 2 AL137793
977 18 2.9 138618 2 AC111060
978 18 2.9 138655 2 AC020447
979 18 2.9 139045 2 AC127021
980 18 2.9 139287 2 AC060794 Homo sapi
981 18 2.9 139370 2 AC136082
982 18 2.9 139444 9 HS380C13
983 18 2.9 139655 2 AC119415
984 18 2.9 139788 2 AC024118
985 18 2.9 140092 9 AC016565 Homo sapi
986 18 2.9 140200 2 AC008961 Homo sapi
987 18 2.9 140201 2 BX511060
988 18 2.9 140476 9 AC104465 Homo sapi
989 18 2.9 140499 2 AC046150
990 18 2.9 141540 9 AL138828 Human DNA
991 18 2.9 141572 2 AC138465 Medicago
992 18 2.9 141672 10 HS142F18
993 18 2.9 141866 9 AL928919 Mouse DNA
994 18 2.9 142087 2 AC092713 Homo sapi
995 18 2.9 142139 2 AC099817 Homo sapi
996 18 2.9 142345 5 AL929053 Zebrafish
997 18 2.9 142439 9 AC008749 Homo sapi
998 18 2.9 143884 2 AC136150 Oryza sat
999 18 2.9 143687 2 AC106793 Homo sapi
1000 18 2.9 143878 9 AC003074 Homo sapi
```

ALIGNMENTS

```
RESULT 1
LOCUS      G04707          254 bp      DNA
DEFINITION human STS WI-4862, sequence tagged site.
ACCESSION  G04707
VERSION    G04707.1 GI:721665
KEYWORDS   STS; STS sequence; primer; sequence tagged site.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
```

REFERENCE
1 (bases 1 to 254)
AUTHORS
Hudson, T.
TITLE
Whitehead Institute/MIT Center for Genome Research; Random Genome
JOURNAL
Unpublished (1995)
AUTHORS
Hudson, T.
TITLE
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped STS
JOURNAL
Unpublished (1995)
COMMENT
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: AAAACATGTTTATTCCTCAGAGA
Primer B: TCTGGAATTTTGTCTAAACACAA
STS size: 202
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3.

FEATURES
source
location/Qualifiers
1..254
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

STS
primer_bind
51..252
/map="804_B_6; 946_D_3; 938_G_10; 951_H_12"

BASE COUNT
complement(228..252)
105 a 34 c 35 g 79 t 1 others
ORIGIN

Query Match 3.5%; Score 22; DB 11; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 228 ATATGCTTATTATTATGTT 249
Db 205 ATATGCTTATTATTATGTT 226

```
RESULT 2
LOCUS      HS12409          108534 bp      DNA
DEFINITION Human DNA sequence from clone RP1-12409 on chromosome 6q21,
ACCESSION  AL021327
VERSION    AL021327.1 GI:2804157
KEYWORDS   HMG.
SOURCE     Homo sapiens (human)
```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 108534)
AUTHORS Phillips, S.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Clone requests: clonerequests@sanger.ac.uk

COMMENT
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep

This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>

RP1-12409 is from the library RP1-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2.

FEATURES
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1..108534
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="RZPD:RP1P704009124"
/db_xref="taxon:9606"
/chromosome="6"
/map="q21"
/clone="RP1-12409"
/clone_lib="RP1-1"
BASE COUNT 34645 a 20919 c 19020 g 33950 t
ORIGIN

Query Match 3.5%; Score 22; DB 9; Length 108534;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

228 ATATGCTTTATTTATTTATGTT 249
|||||
Db 16369 ATATGCTTTATTTATTTATGTT 16390

RESULT 3
AC141496/c 127699 bp DNA linear HTG 24-MAR-2003
LOCUS Rattus norvegicus clone CH230-511K8, WORKING DRAFT SEQUENCE, 8
DEFINITION unorderd pieces.
AC141496
AC141496.2 GI:29165563
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 127699)
AUTHORS Muzny, D., Marle, M., Metker, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Bacc, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnes, M., Barnham, F., Bismato, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bunay, C., Burck, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denon, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durkin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorjis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loushewa, L., Louised, H., Lozano, R., Lu, X., Ma, J., Maheshwari, M., Mahdairne, M., Mahmoud, M., Malloy, K., Mangum, B., Mapur, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Mirza, E., Montemayor, U., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokelembu, O., Okwou, G., Olarnpasagoon, A., Pal, S., Parks, K., Patel, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Pu, L., Quirio, J., Rechlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C.D., Smaiz, D., Speed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Woodden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 127699)
Submitted (17-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 127699)
Worley, K.C.
Direct Submission
Submitted (24-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 24, 2003 this sequence version replaced gi:28975757.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

```

----- Project Information
Center project name: KEGG
Center clone name: CH230-511K8
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124484 bases at least Q40
Consensus quality: 125345 bases at least Q30
Consensus quality: 125900 bases at least Q20
Estimated insert size: 126226; sum-of-coverage estimation
Quality coverage: 5x in Q20 bases; sum-of-coverage estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1805: contig of 1805 bp in length
* 1806 1905: gap of unknown length
* 1906 4652: contig of 2747 bp in length
* 4653 4752: gap of unknown length
* 4753 8159: contig of 3407 bp in length
* 8160 8259: gap of unknown length
* 8260 13974: contig of 5715 bp in length
* 13975 14074: gap of unknown length
* 14075 22226: contig of 8152 bp in length
* 22227 22326: gap of unknown length
* 22327 41656: contig of 19330 bp in length
* 41657 41757: gap of unknown length
* 41757 78480: contig of 36724 bp in length
* 78481 78580: gap of unknown length
* 78581 127699: contig of 49119 bp in length.
*
FEATURES
source
1..127699
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-511K8"

BASE COUNT
40596 a 22414 c 23032 g 40955 t 702 others

ORIGIN
Query Match 3.5%; Score 22; DB 2; Length 127699;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 180 CTATATTTTACGATCATTT 201
Db 126250 CTATATTTTACGATCATTT 126229

RESULT 4
AL135926/c
LOCUS
DEFINITION
AL135926 158519 bp DNA linear PRI 30-NOV-2000
Human DNA sequence from clone RP11-375F2 on chromosome 1 contains a
pseudogene similar to Ubql (ubiquitin-like 1 (sentrin)), a
pseudogene similar to ribosomal protein L29, ESTs, STSs and GSSs,
complete sequence.
ACCESSION
AL135926
VERSION
AL135926.12 GI:9801286
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 158519)
Chapman, J.
Direct Submission
TITLE

```

JOURNAL

COMMENT

Submitted (03-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone Requesters: clonerequest@sanger.ac.uk

On Aug 14, 2000 this sequence version replaced gi:9621473. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human Chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>

RP11-375F2 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR.paces.6>

IMPORTANT: This sequence is not the entire insert of clone RP11-375F2 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-375F2 is at 158519 in this sequence. The true right end of clone RP1-10C16 is at 100 in this sequence.

```

FEATURES
source
1..158519
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-375F2"
/clone="RP1-10C16"
/clone="RPCI-11.2"
460..675
/note="WTLTJ repeat: matches 306..514 of consensus"
1465..1514
/note="25 copies 2 mer to 72% conserved"
1775..1824
/note="WIR repeat: matches 85..135 of consensus"
3415..3734
/note="L2 repeat: matches 2373..2707 of consensus"
4294..5519
/note="L1MB7 repeat: matches 4938..6173 of consensus"
5535..5640
/note="L1MB5 repeat: matches 5322..5428 of consensus"
5652..5945
/note="Alusd repeat: matches 12..309 of consensus"
5960..5995
/note="9 copies 4 mer aagg 88% conserved"
5997..6055
/note="L1MB5 repeat: matches 5413..5471 of consensus"
6061..6158
/note="Alu repeat: matches 214..311 of consensus"
6160..6855
/note="L1MB5 repeat: matches 5460..6168 of consensus"
6919..7101
/note="L2 repeat: matches 2206..2403 of consensus"
7099..7228
/note="L2 repeat: matches 2620..2750 of consensus"
7828..8069
/note="WER46A repeat: matches 2..235 of consensus"
8185..8469
/note="Alusx repeat: matches 1..285 of consensus"

```

```

repeat_region      8551..8624
                    /note="MIR repeat: matches 81..153 of consensus"
misc_feature        8951..9347
                    /note="match: GSS: Em:B40536"
repeat_region      10287..10464
                    /note="MIR repeat: matches 28..215 of consensus"
repeat_region      10588..11321
                    /note="L1P8 repeat: matches 5371..6158 of consensus"
repeat_region      11337..11671
                    /note="MLTID repeat: matches 13..381 of consensus"
repeat_region      11672..11971
                    /note="Alu repeat: matches 1..295 of consensus"
misc_feature        11855..12218
                    /note="unidirectional dGTP only"
repeat_region      11972..12090
                    /note="MLTID repeat: matches 381..492 of consensus"
repeat_region      12106..12403
                    /note="AluX repeat: matches 1..297 of consensus"
repeat_region      12419..13151
                    /note="L2 repeat: matches 1683..2403 of consensus"
misc_feature        13091..13572
                    /note="match: GSS: Em:AQ087510"
repeat_region      13164..13253
                    /note="L2 repeat: matches 2576..2669 of consensus"
repeat_region      13254..13403
                    /note="75 copies 2 mer at 76% conserved"
repeat_region      13267..13410
                    /note="24 copies 6 mer tatata 78% conserved"
repeat_region      13654..13742
                    /note="MLTIE repeat: matches 2..81 of consensus"
repeat_region      14045..14226
                    /note="MLTIE repeat: matches 385..567 of consensus"
misc_feature        complement(14529..15003)
                    /note="match: GSS: Em:AQ798857"
misc_feature        14901..15366
                    /note="match: GSS: Em:AQ221861"
repeat_region      15371..15463
                    /note="MIR repeat: matches 60..153 of consensus"
repeat_region      16536..16633
                    /note="L1M4 repeat: matches 3093..3194 of consensus"
repeat_region      16839..17215
                    /note="L1P7 repeat: matches 5767..6143 of consensus"
repeat_region      17225..17961
                    /note="L1P3 repeat: matches 5410..6146 of consensus"
repeat_region      17962..19671
                    /note="L1P7 repeat: matches 4077..5788 of consensus"
repeat_region      19672..20271
                    /note="L1P7 repeat: matches 3477..4076 of consensus"
repeat_region      20277..20462
                    /note="L1M4 repeat: matches 3403..3585 of consensus"
repeat_region      20479..21023
                    /note="L1P8 repeat: matches -1540..-1003 of consensus"
repeat_region      21083..22136
                    /note="L1P8 repeat: matches -977..1014 of consensus"
repeat_region      22104..24249
                    /note="L1M2 repeat: matches 37..2571 of consensus"
repeat_region      24175..24890
                    /note="L1 repeat: matches 2118..2843 of consensus"
repeat_region      24896..25532
                    /note="L1M1 repeat: matches 5508..6163 of consensus"
repeat_region      25865..25900
                    /note="6 copies 6 mer TGTGT 97% conserved"
repeat_region      25903..26184
                    /note="Alu repeat: matches 1..282 of consensus"
misc_feature        27110..27647
                    /note="match: STS: Em:HS045M12S"
repeat_region      27233..27346
                    /note="L2 repeat: matches 2549..2668 of consensus"
repeat_region      27347..27437
                    /note="L2 repeat: matches 2064..2155 of consensus"
repeat_region      27438..27487
                    /note="L1M/C/D repeat: matches 5637..5685 of consensus"
repeat_region      27552..27933

```

```

repeat_region      27982..28315
                    /note="L1M/C4 repeat: matches 6621..7006 of consensus"
repeat_region      28256..28552
                    /note="L1M/C4 repeat: matches 7094..7422 of consensus"
repeat_region      28629..28938
                    /note="L1M/C5 repeat: matches 7262..7589 of consensus"
repeat_region      29045..29218
                    /note="Alu repeat: matches 1..310 of consensus"
repeat_region      30188..30300
                    /note="L1M1 repeat: matches 5338..5450 of consensus"
repeat_region      30761..30877
                    /note="MIR repeat: matches 71..190 of consensus"
repeat_region      31253..31494
                    /note="L2 repeat: matches 2362..2474 of consensus"
repeat_region      31722..33025
                    /note="L2 repeat: matches 466..712 of consensus"
gene                /gene="BA375F2.1"
                    /pseudo
CDS                 31722..33025
                    /gene="BA375F2.1"
                    (similar to UBL1 (ubiquitin-like 1
                    (sentrin)))
                    match: cDNAs: Em:U72722
                    match: ESTs: Em:A191222 Em:A1248769
                    match: proteins: Tr:Q9PT08 Tr:O23759 Sw:P55853 Tr:Q92172
                    Sw:Q93068 Sw:P55854 Sw:P55855 Sw:O13351 Sw:O12306
                    Tr:O97102 Tr:O57686"
                    /pseudo
                    /codon_start=1
                    /evidence=not_experimental
                    complement(32129..32630)
                    /note="match: GSS: Em:AQ747371"
                    32225..32619
                    /note="match: GSS: Em:AQ093192"
                    complement(32404..32630)
                    /note="match: GSS: Em:AQ195587"
                    33174..33222
                    /note="L2 repeat: matches 2624..2668 of consensus"
                    repeat_region      33291..33725

Query Match      3.5%; Score 22; DB 9; Length 158519;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      163 TTTGAACAATTTCTACTATA 184
Db      103720 TTTGAACAATTTCTACTATA 103699

RESULT 5
AC141118
LOCUS      AC141118      160961 bp      DNA      linear      HTG 27-MAR-2003
DEFINITION      Rattus norvegicus clone CH230-525P6, WORKING DRAFT SEQUENCE, 40
unordered pieces.
ACCESSION      AC141118
VERSION      AC141118.2 GI:28913318
KEYWORDS      HTG: HTGS PHASE1; HTGS DRAFT.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 160961)
REFERENCE
AUTHORS      Murny,D,Marie.,Metzker,M,Lee.,Abramzon,S.,Adams,C.,Alder,J.,
Allen,C.,Allen,H.,Albrooks,S.,Amin,A.,Anguiano,D.,
Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
Baldwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
Biewald,K.,Blair,D.,Blankenbury,K.,Blyth,P.,Brown,M.,
Bryant,N.,Buhay,C.,Burch,P.,Burrell,K.,Calderon,E.,
Cardenas,V.,Carter,K.,Cavazos,I.,Ceasar,H.,Center,A.,
Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,
Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,
Davila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,

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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Geisegorsky, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Huliy, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., Kang, L., Kovar, C., Kows, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheva, L., Louisedge, H., Lozano, R.J., Lu, X., Ma, T., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Manning, S., McLeod, M., McNeill, T., Meenan, E., Miosavljovic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackeleme, O., Okunnu, G., Olarunpusagbon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X., Z., Sorrelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valae, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlaczky, R., Wooten, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 160961)
Worley, K.C.

Direct Submission
Submitted (09-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 160961)
Worley, K.C.

Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 11, 2003 this sequence version replaced gi:28935584.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: KES0
Center clone name: CH230-525P6

Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap version 0.990329
Consensus quality: 149125 bases at least Q40
Consensus quality: 153679 bases at least Q30
Consensus quality: 157936 bases at least Q20
Estimated insert size: 153783; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1574: contig of 1574 bp in length
1575 1674: gap of unknown length
1675 3680: contig of 206 bp in length
3681 3780: gap of unknown length
3781 5079: contig of 1299 bp in length
5080 5179: gap of unknown length
5180 7286: contig of 2107 bp in length
7287 7385: gap of unknown length
7387 9577: contig of 2191 bp in length
9578 9677: gap of unknown length
9678 11965: contig of 2288 bp in length
11966 12065: gap of unknown length
12066 14080: contig of 2015 bp in length
14081 14180: gap of unknown length
14181 15944: contig of 1764 bp in length
15945 16044: gap of unknown length
16045 18936: contig of 2892 bp in length
18937 19036: gap of unknown length
19037 21532: contig of 2496 bp in length
21533 21632: gap of unknown length
21633 24022: contig of 2390 bp in length
24023 24122: gap of unknown length
24123 25620: contig of 1498 bp in length
25621 27462: contig of 1742 bp in length
27463 27562: gap of unknown length
27563 30387: contig of 2825 bp in length
30388 30487: gap of unknown length
30488 33253: contig of 2766 bp in length
33254 33353: gap of unknown length
33354 35321: contig of 1968 bp in length
35322 35421: gap of unknown length
35422 38319: contig of 2898 bp in length
38320 38419: gap of unknown length
38420 41618: contig of 3199 bp in length
41619 41718: gap of unknown length
41720 44430: contig of 2712 bp in length
44431 44530: gap of unknown length
44531 47279: contig of 2749 bp in length
47280 47380: gap of unknown length
47381 52261: contig of 4882 bp in length
52262 52361: gap of unknown length
52362 54608: contig of 2247 bp in length
54609 54708: gap of unknown length
54709 57077: contig of 2999 bp in length
57078 57807: gap of unknown length
57808 60363: contig of 2556 bp in length
60364 60463: gap of unknown length
60464 63938: contig of 3475 bp in length
63939 64038: gap of unknown length
64039 67104: contig of 3066 bp in length
67105 71066: gap of unknown length
71067 71667: contig of 4462 bp in length
71668 76309: contig of 4543 bp in length
76310 76410: gap of unknown length
76411 81082: contig of 4673 bp in length
81083 81182: gap of unknown length
81183 84621: contig of 3439 bp in length
84622 89922: contig of 5271 bp in length
89923 90092: gap of unknown length
90093 95597: contig of 5505 bp in length
95598 95697: gap of unknown length
95698 100812: contig of 5115 bp in length

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* 100813 100912: gap of unknown length
* 100913 106321: contig of 5409 bp in length
* 106322 106421: gap of unknown length
* 106422 113989: contig of 7568 bp in length
* 113990 114089: gap of unknown length
* 114090 120489: contig of 6400 bp in length
* 120490 120589: gap of unknown length
* 120590 127231: contig of 6642 bp in length
* 127232 127331: gap of unknown length
* 127332 135054: contig of 7723 bp in length
* 135055 135154: gap of unknown length
* 135155 146623: contig of 11469 bp in length
* 146624 160961: contig of 14238 bp in length.
* 146724 160961: contig of 14238 bp in length.

FEATURES
  source
    1. 160961
       /organism="Rattus norvegicus"
       /mol_type="genomic DNA"
       /db_xref="taxon:10116"
       /clone="CH230-525P6"

BASE COUNT  52694 a 28129 c 28611 g 47601 t 3926 others

ORIGIN
Query Match      3.5%; Score 22; DB 2; Length 160961;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy  180 CTATTTTTCAGATCATTT 201
Db  113195 CTATTTTTCAGATCATTT 113216

RESULT 6
BX296535/c 164604 bp DNA linear HTG 02-JUN-2003
LOCUS      Dario rerio clone CH211-234P1, *** SEQUENCING IN PROGRESS ***, 5
DEFINITION unorderd pieces.
ACCESSION  BX296535
VERSION    BX296535.2 GI:30348616
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE     Dario rerio (zebrafish)
ORGANISM   Dario rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
            Cypriniformes; Cyprinidae; Danio.
            1 (bases 1 to 164604)
REFERENCE  1 (bases 1 to 164604)
AUTHORS   McJaren, S.
TITLE     Direct Submission
JOURNAL   Submitted (28-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
            On May 2, 2003 this sequence version replaced gi:29335436.

COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zc334P1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 163108 bases at least Q40
Consensus quality: 163466 bases at least Q30
Consensus quality: 163645 bases at least Q20
Insert size: 164204; sum-of-contigs
Insert size: 159749; 15.3% error; agarose-fp
Quality coverage: 6.58x in Q20 bases; sum-of-contigs Quality
coverage: 6.91x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is

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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 36553: contig of 36553 bp in length
* 36554 36653: gap of 100 bp
* 36654 58304: contig of 21651 bp in length
* 58305 58404: gap of 100 bp
* 58405 132711: contig of 74307 bp in length
* 132712 132811: gap of 100 bp
* 132812 147096: contig of 14285 bp in length
* 147097 147197: gap of 100 bp
* 147197 164604: contig of 17408 bp in length.

FEATURES
  source
    1. 164604
       /organism="Dario rerio"
       /mol_type="genomic DNA"
       /db_xref="taxon:7955"
       /clone="CH211-234P1"
       /clone_1pb="CHOR-211"

BASE COUNT  51202 a 30712 c 30580 g 51710 t 400 others

ORIGIN
Query Match      3.5%; Score 22; DB 2; Length 164604;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy  169 ACAATTTTCTACTATTTT 190
Db  141836 ACAATTTTCTACTATTTT 141815

RESULT 7
AL356425/c 183901 bp DNA linear HTG 10-JUL-2001
LOCUS      Homo sapiens chromosome 6 clone RP11-390H10, *** SEQUENCING IN
DEFINITION PROGRESS ***, 14 unorderd pieces.
ACCESSION  AL356425
VERSION    AL356425.5 GI:9863770
KEYWORDS  HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1
REFERENCE  1
AUTHORS   Slim, S.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone
            requests: clonerequests@sanger.ac.uk
            On Aug 21, 2000 this sequence version replaced gi:9213882.
            -----
            Genome Center
Center: Sanger Centre

```


Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: hunguery@sanger.ac.uk

 Project Information
 Center project name: BA390H10

 Summary Statistics
 Sequencing program: XGAP4; version 4.5
 Sequencing vector: Plasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 43% of reads
 Chemistry: Dye-terminator ABI; 13% of reads
 Chemistry: Dye-primer-amerham; 42% of reads
 Consensus quality: 176464 bases at least Q40
 Consensus quality: 179210 bases at least Q30
 Consensus quality: 180657 bases at least Q20
 Insert size: 182601; sum-of-contigs
 Insert size: 195711; 10.1% error; agarose-fp
 Quality coverage: 6.80x in Q20 bases; sum-of-contigs Quality
 Coverage: 8.70x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 14 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1      4652: contig of 4652 bp in length
*      4653      4752: gap of 100 bp
*      4753      10980: contig of 6228 bp in length
*      10981      11080: gap of 100 bp
*      11081      23147: contig of 12067 bp in length
*      23148      23247: gap of 100 bp
*      23248      26829: contig of 3582 bp in length
*      26830      26929: gap of 100 bp
*      26930      29454: contig of 2525 bp in length
*      29455      29554: gap of 100 bp
*      38902      38902: contig of 9348 bp in length
*      38903      39002: gap of 100 bp
*      39003      150562: contig of 111560 bp in length
*      150563      150662: gap of 100 bp
*      150663      153078: contig of 2416 bp in length
*      153079      153178: gap of 100 bp
*      153179      158533: contig of 5355 bp in length
*      158534      158633: gap of 100 bp
*      161010      161010: contig of 2377 bp in length
*      161101      161111: gap of 100 bp
*      161111      164104: contig of 2994 bp in length
*      164105      164204: gap of 100 bp
*      164205      173216: contig of 9012 bp in length
*      173217      173316: gap of 100 bp
*      173317      178295: contig of 4979 bp in length
*      178296      178395: gap of 100 bp
*      178396      183901: contig of 5506 bp in length.
  
```

FEATURES

```

source
  1..183901
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"
    /chromosome="6"
    /clone="RP11-390H10"
    /clone_11b="RP11-11.2"
    1..4652
      /note="assembly_fragment:03969
      clone_end:77
      vector_side:left"
      4753..10980
        /note="assembly_fragment:00460
        fragment_chain:1"
        11081..23147
          /note="assembly_fragment:00746
          fragment_chain:1"
        23248..26829
  
```

```

misc_feature /note="assembly_fragment:04384
             fragment_chain:2"
             26930..29454
             /note="assembly_fragment:01338
             fragment_chain:2"
             29555..38902
             /note="assembly_fragment:00073.0"
             39003..150562
             /note="assembly_fragment:00200.0"
             150663..153078
             /note="assembly_fragment:00219"
             153179..158533
             /note="assembly_fragment:00251"
             158634..161010
             /note="assembly_fragment:00513"
             161111..164104
             /note="assembly_fragment:01982"
             164205..173216
             /note="assembly_fragment:02741"
             173317..178295
             /note="assembly_fragment:02844"
             178396..183901
             /note="assembly_fragment:03632"
misc_feature misc_count 57024 a 32652 c 34405 g 58512 t 1304 others
BASE COUNT
ORIGIN
Query Match 3.5%; Score 22; DB 2; Length 183901;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
```

```

Oy 228 ATATGCTTATTTATTTATGTT 249
Db 131164 ATATGCTTATTTATTTATGTT 131163
  
```

```

RESULT 8
AC135412
LOCUS
DEFINITION
  Rattus norvegicus clone CH230-4M1, *** SEQUENCING IN PROGRESS ***,
  10 unordered pieces.
ACCESSION
  AC135412.3 GI:30466364
VERSION
  HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS
  Rattus norvegicus (Norway rat)
SOURCE
  ORGANISM
    Rattus norvegicus
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
      Rattus.
  
```

REFERENCE

AUTHORS

1 (bases 1 to 250935)
 Muzny, D., Marie, Metzker, M., Lee, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsebrook, S., Amin, A., Angiano, D.,
 Anyalbechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Biewald, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrill, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
 Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
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 Georegeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
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 Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorensbuewa, L., Louised, H., Lozado, R. J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mathew, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Munnada, M., Murphy, M., Natr, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwoketlemoh, O., Okwou, G., Olarnunagoon, A., Pal, S., Parks, K.,
 Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
 Plopper, F., Poldexer, A., Popovic, D., Prims, E., Pu, L.,
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 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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 Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
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 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
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 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemari, K.,
 Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wiczak, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstock, G., and Gibbs, R. A.
 Unpublished
 Direct Submission
 2 (bases 1 to 250935)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (15-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 250935)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On May 9, 2003 this sequence version replaced gi:24942076.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GAXY
 Center clone name: CH230-4M1
 ----- Summary Statistics
 Assembly program: Atlas;
 Consensus quality: 14854 bases at least Q40
 Consensus quality: 15473 bases at least Q20
 Consensus quality: 15832 bases at least Q20
 Estimated insert size: 147873; sum-of-contigs estimation
 Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Gendm_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 5743: contig of 5743 bp in length
 * 5744 5843: gap of unknown length
 * 5844 44807: contig of 3864 bp in length
 * 44808 44907: gap of unknown length
 * 44908 51228: contig of 6321 bp in length
 * 51229 51328: gap of unknown length
 * 51329 230560: contig of 179232 bp in length
 * 23061 230660: gap of unknown length
 * 23061 234274: contig of 3614 bp in length
 * 234275 234374: gap of unknown length
 * 234375 245739: contig of 11365 bp in length
 * 245740 245839: gap of unknown length
 * 245840 245869: contig of 1030 bp in length
 * 245870 245969: gap of unknown length
 * 245970 248471: contig of 1502 bp in length
 * 248472 248571: gap of unknown length
 * 248572 248572: contig of 1181 bp in length
 * 249753 249852: gap of unknown length
 * 249853 250935: contig of 1083 bp in length.

FEATURES
 source
 1..250935
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-4M1"
 1..1739
 /note="wgs contig"
 5844..7590
 /note="wgs contig"
 41966..44807
 /note="wgs contig"
 44908..47234
 /note="wgs contig"
 116578..117961
 /note="wgs contig"
 209111..210845
 /note="wgs contig"
 218123..220132
 /note="wgs contig"
 234375..235653
 /note="wgs contig"
 54579 a 29101 c 28918 g 48007 t 90330 others
 BASE COUNT
 ORIGIN
 Query Match 3.5%; Score 22; DB 2; Length 250935;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTATATTTTACAGATCATTT 201
 DB 24484 CTATATTTTACAGATCATTT 244505

 RESULT 9
 LOCUS AC096515/c
 DEFINITION Rattus norvegicus clone CH230-5A2, *** SEQUENCING IN PROGRESS ***,
 9 unordered pieces.
 ACCESSION AC096515
 VERSION AC096515.5 GI:24818491
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 286790)
 REFERENCE
 AUTHORS Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alshrocks, S., Amin, A., Anguitano, D., Anyia, E., Becht, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Ccenter, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Day-Carroll, L., De Anda, C., Deedrich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinb, H., Diya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganea, R., Garcia, A., Garner, T., Garza, M., Gebregergs, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havjak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hui, S., Hume, J., Idlebird, D., Jackson, A., Jackson, J., Jacob, L., Jiang, H., Johnson, R., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Lervan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheaw, L., Louised, H., Lozada, R.J., Lu, X., Ma, U., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenan, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Morgan, M., Morris, K., Morris, S., Munday, M., Murphy, M., Nait, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelam, O., Okunnu, G., Olarinmugson, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plapper, F., Polindexter, A., Popovic, D., Prims, E., Pu, L., Puazo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reish, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.U., Sanders, W., Savery, G., Scherer, S., Scott, G., Shattman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Slater, C.D., Smajz, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingay, A., Trejos, Z., Uman, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, R., Wiczek, R., Wood, H., Wotley, K., Williams, G., Willson, R., Wleczek, R., Wei, X., White, F., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 286790)
Worley, K.C.

Direct Submission
Submitted (18-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 286790)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:227272011.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome

```

shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GAZY
Center clone name: CH230-5A2
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 79420 bases at least Q40
Consensus quality: 83499 bases at least Q30
Consensus quality: 86426 bases at least Q20
Estimated insert size: 70782; sum-of-contigs estimation
Quality coverage: 5x in Q20 Bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 216997: contig of 216997 bp in length
* 216998 217097: gap of unknown length
* 217098 246339: contig of 31242 bp in length
* 248340 248439: gap of unknown length
* 248440 258863: contig of 10424 bp in length
* 258864 258963: gap of unknown length
* 258964 263216: contig of 4253 bp in length
* 263217 263317: gap of unknown length
* 263318 281803: contig of 18487 bp in length
* 281804 281903: gap of unknown length
* 281904 283051: contig of 1148 bp in length
* 283052 283151: gap of unknown length
* 283152 284195: contig of 1044 bp in length
* 284196 284295: gap of unknown length
* 284296 285440: contig of 1145 bp in length
* 285441 285540: gap of unknown length
* 285541 286790: contig of 1250 bp in length.
*
* Location/Qualifiers
* 1. 286790
* /organism="Rattus norvegicus"
* /mol_type="genomic DNA"
* /db_xref="taxon:101116"
* /clone="CH230-5A2"
* 2439..2951
*
misc_feature
/note="clone_boundary
clone_end:T7
site:ECORI
end_sequence:BH334013"
19424..20864
/note="wgs_contig"
175176..175894
/note="clone_boundary
clone_end:Sp6
site:ECORI
end_sequence:BH334015"
177823..179284
/note="wgs_end_extension
clone_end:Sp6"
183835..184861
/note="wgs_end_extension
clone_end:Sp6"
185363..186393
/note="wgs_end_extension
clone_end:Sp6"
197893..199394

```

```
BASE COUNT      29868 a 15794 c 16225 g 26866 t 198037 others
ORIGIN
misc_feature     /note="wgs_end_extension
                  clone_end:Sp6"
                  215431..216997
/note="wgs_end_extension
clone_end:Sp6"
217098..218581
/note="wgs_end_extension
clone_end:Sp6"
220322..221556
/note="wgs_end_extension
clone_end:Sp6"
246596..248339
/note="wgs_end_extension
clone_end:Sp6"
248440..249824
/note="wgs_end_extension
clone_end:Sp6"
258964..260512
/note="wgs_end_extension
clone_end:Sp6"
266700..269279
/note="wgs_end_extension
clone_end:Sp6"
273808..275227
/note="wgs_end_extension
clone_end:Sp6"
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Query Match	Score	DB	Length
Best Local Similarity	100.0%	Pred. No. 1.2	
Matches	22	Conservative	0
		Mismatches	0
		Indels	0
		Gaps	0

Qy	180	CTATATTTTTCAGATCATTT	201
Db	267793	CTATATTTTTCAGATCATTT	267772

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	BASE COUNT	ORIGIN								
AC013856	Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.	AC013856	AC013856.1	GI:6437479	HTG; HTGS_PHASE2.	Drosophila melanogaster (fruit fly)	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	1 (bases 1 to 44284)	Adams, M. and Venter, J.C.	Direct Submission	Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA	This sequence was identified as CDM:10211564 by the submitter. For further information on this sequence e-mail to fly@celera.com.	* NOTE: This is a 'working draft' sequence.	* This sequence will be replaced	* by the finished sequence as soon as it is available and	* the accession number will be preserved.	Location/Qualifiers	1..44284	/organism="Drosophila melanogaster"	/mol_type="genomic DNA"	/db_xref="taxon:7227"	13028 a 9444 c 9570 g 12242 t

```
Query Match      3.4%; Score 21; DB 2; Length 44284;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	345	TACCAAGGTTTTTAAATTAA	365
Db	40289	TACCAAGGTTTTTAAATTAA	40309

LOCUS	AC020373	60164 bp	DNA	linear	HTG 03-JAN-2000
DEFINITION	Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.				
ACCESSION	AC020373				
VERSION	AC020373.1 GI:6664524				
KEYWORDS	HTG; HTGS PHASE2.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 60164)				
AUTHORS	Adams,M. and Venter,J.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA.				
COMMENT	This sequence was identified as CDM:10212952 by the submitter. For more information on this record e-mail to fly@celera.com.				
	* NOTE: This is a 'working draft' sequence.				
	* This sequence will be replaced				
	* by the finished sequence as soon as it is available and				
	* the accession number will be preserved.				

```

source          1..60164
                /organism="Hirotophila melanogaster"
                /mol_type="genomic DNA"
                /db_xref="taxon:7227"
BASE COUNT      17290 a 12604 c 17386 t
ORIGIN
Query Match     3.4%; Score 21; DB 2; Length 60164;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY             504 AACCTTTACCAATTATATTA 524
                |||
Db              39804 AACCTTTACCAATTATATTA 39824

```

RESULT 12
AL671966/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AL671966 61913 bp DNA linear PRI 07-FEB-2002
Human AL671966.LI445924
sequence.
AL671966.1 GI:18642415
HTC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 61913)
Griffiths, C.
Direct Submission
Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humgen@wanger.ac.uk Clone requests: clonequest@sanger.ac.uk
On Feb 8, 2002 this sequence version replaced gi.11375014.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>. RP11-544L8 is from the library RP11-2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>.
 VECTOR: pBACe3.6
 IMPORTANT: This sequence is not the entire insert of clone RP11-544L8. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-544L8 is at 1 in this sequence. The true left end of clone RP1-249H1 is at 61814 in this sequence.

FEATURES

source

```
1..61913
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-544L8"
/clone_1lb="RP11-2"
/clone_1lb="RP11-2"
BASE COUNT      19670 a 11945 c 11807 g 18491 t
ORIGIN
```

```
Query Match      3.4%; Score 21; DB 9; Length 61913;
Best Local Similarity 100.0%; Pred.No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      272 TGATGCCAATATTACTTTTAA 292
          |||||
Db      26512 TGATGCCAATATTACTTTTAA 26492
```

```
RESULT 13
HS341D10/c
LOCUS      HS341D10      82517 bp. DNA linear PRI 13-DEC-2001
DEFINITION Human DNA sequence from clone RP3-341D10 on chromosome X contains a
             gene for a novel protein, part of the gene for a protein similar to
             ADP ribosylation factor 3, part of a gene similar to HTP9c and a
             Cpg island, complete sequence.
ACCESSION  Z97985
VERSION    Z97985.16 GI:10178309
KEYWORDS  HTG; ADP; Cpg island.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 82517)
Clark G.
```

```
REFERENCE   Direct Submission
AUTHORS    Submitted (12-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
TITLE      Cambridgehire, CH10 1SA, UK. E-mail enquiries:
JOURNAL    humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Sep 15, 2000 this sequence version replaced gi:10120292.
```

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; information on the WORMPEP database can be found at

FEATURES

source

http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX>. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP3-341D10 is from the library RP11-3 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>.
 VECTOR: pCYPAC2
 IMPORTANT: This sequence is not the entire insert of clone RP3-341D10. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP3-341D10 is at 82517 in this sequence. The true left end of clone RP5-1053B6 is at 47109 in this sequence. The true right end of clone RP1-146H1 is at 20342 in this sequence. The true right end of clone DL0XNC01-131B10 is at 100 in this sequence.

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Location/Qualifiers
1..82517
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP3-341D10"
/clone_1lb="RP1-3"
/clone_1lb="RP1-3"
2573..32600
/note="14 copies 2 mer tg 96% conserved"
complement(5744..6585)
/note="match: GSS: Em:A0897607"
5903..6593
/note="LTR33 repeat: matches 1..521 of consensus"
complement(5994..6593)
/note="match: GSS: Em:A0282846"
7799..8818
/note="L1MD repeat: matches 27..1017 of consensus"
9132..9697
/note="L1MD repeat: matches 1017..1590 of consensus"
15403..15831
/note="L1P11 repeat: matches 5725..6161 of consensus"
16674..18783
/gene="AJ341D10.1"
16674..18783
/gene="AJ341D10.1"
/product="AJ341D10.1 (novel protein)"
/note="match: CDNAS: Em:AF116666 Em:AL157483 Em:AK002126
match: ESTs: Em:D62659 Em:AW007673 Em:AA410548 Em:AM264439
Em:D61822 Em:AL049046 Em:C01580 Em:A1652628 Em:A1110652
Em:D62752 Em:D82671 Em:AW026446 Em:AA773203 Em:AM581342
Em:AW088009 Em:AW025693 Em:A1699487 Em:AA281222
Em:AW440954 Em:A1282011 Em:AA715822 Em:AA079045
Em:AW659871 Em:AP063526 Em:AA043597 Em:Z45941 Em:A1913223
Em:AL049045 Em:A1640527 Em:A1990225 Em:A1356844
Em:AW471241 Em:A1922789 Em:H13398 Em:D79651"
/feature="not experimental"
16674..17003
/gene="AJ341D10.1"
/note="match: proteins: Tr:Q9VXS9 Tr:O02330 Tr:Q9Y2U5
Tr:Q9V517"
/codon_start=1
/evidence="not experimental"
/product="AJ341D10.1 (novel protein)"
/protein_id="CAD19074.1"
/db_xref="GI:17736645"
/translacion="VTCQYRSDFLIGRFMEVKMGSGEDVHLCKQYIHGDIIVITWP
VTGIFHMLPERCADELPFOYRMCIOSKAINESRSHLGMVFEFEIETLHLKQAYR
TNSBAVG"
```

CDS

```

polyA_signal      18778..18783
                  /gene="dJ341D10.1"
repeat_region     20672..20723
                  /note="26 copies 2 mer aa 73% conserved"
repeat_region     22455..22572
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repeat_region     23789..25430
                  /note="WSTA-internal repeat: matches 2..1651 of consensus"
repeat_region     26627..26777
                  /note="MER58C repeat: matches 44..87 of consensus"
repeat_region     30005..30234
                  /note="MER8 repeat: matches 1..237 of consensus"
misc_feature      31771..32971
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misc_feature      32175..33183
                  /note="1372bp of IS186 (X03123) excised: This sequence
                  represents the duplicated flanking sequence of the IS186."
                  32299
misc_feature      /note="Tandem repeat. Forced join. Gap size estimated to
                  be approximately 850bp by BAMH1 and ECOR1 restriction
                  enzyme digest data."
misc_feature      /note="Tandem repeat. Single clone region"
                  complement(32350..32388)
misc_feature      /note="match: GSS: Em:AQ473058"
                  33793..33848
repeat_region     /note="28 copies 2 mer tc 73% conserved"
                  36506..36833
repeat_region     /note="L1M43 repeat: matches 5975..6300 of consensus"
                  37145..37613
repeat_region     /note="L1M43 repeat: matches 5499..5975 of consensus"
                  41221..41505
misc_feature      /note="match: STS: Em:G04625"
                  41932..41973
repeat_region     /note="21 copies 2 mer aa 78% conserved"
                  42358..42856
misc_feature      /note="match: GSS: Em:B99529"
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                  /codon_start=3
                  /evidence=not_experimental
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                  3)"
                  /protein_id="CAD19075.1"
                  /db_xref="GI:17736646"
                  /translation="LPSKTDHCKMSKELTTLLDREYELSIYDNGDLKGRAMPYVYAO
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misc_feature      47478..47613
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misc_feature      47953..48394
                  /note="match: GSS: Em:AQ725887"
repeat_region     48316..48343
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repeat_region     51272..51632
                  /note="L1M44 repeat: matches 5892..6289 of consensus"
misc_feature      52831..53269
                  /note="match: GSS: Em:AQ210994"
                  complement(53421..53946)
misc_feature      /note="match: GSS: Em:A0666679"
                  53958..54526
misc_feature      /note="match: GSS: Em:AQ483633"
                  55574..56018
repeat_region     /note="L1M44 repeat: matches 5833..6294 of consensus"
                  61332..61798
repeat_region     /note="UTR32 repeat: matches 15..471 of consensus"
                  63634..63884
repeat_region     /note="AluI/mcmonmer repeat: matches 249..299 of consensus"
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repeat_region     /note="TIGGER1 repeat: matches 2174..2410 of consensus"
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gene              /note="MER74B repeat: matches 128..548 of consensus"
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mRNA              /gene="dJ341D10.3"
                  /note="join(69768..70171,78435..78534,78748..78867,
                  79951..80026,80467..80779,81432..>81526))"
                  /gene="dJ341D10.3"
                  /product="dJ341D10.3 (similar to HpaII tiny fragments
                  locus 9C (HTF9C))"
                  /note="match: cDNAs: Em:X56044
                  match: ESTs: Em:W39709 Em:A1192958 Em:AA749428 Em:AA721368
                  Em:AA373290 Em:W15487 Em:W52823 Em:A1765573 Em:AA091456"
                  /evidence=not_experimental
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                  79951..80026,80467..80779,81432..>81526))
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                  /note="match: proteins: Tr:P70222"
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                  /evidence=not_experimental
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                  locus 9C (HTF9C))"
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Query Match      3.4%; Score 21; DB 9; Length 82517;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY              173 TTTTCTACTATATTTTACAG 193
Db              70852 TTTTCTACTATATTTTACAG 70832

RESULT 14
AC005449
LOCUS            AC005449
DEFINITION      AC005449 85518 bp DNA linear INV 23-DEC-1998
                  Drosophila melanogaster, chromosome 2R, region 44C4-44C5, Pl clone
                  D506765, complete sequence.
ACCESSION       AC005449
VERSION         AC005449.1 GI:4056408
KEYWORDS        HTG.
SOURCE          Drosophila melanogaster (fruit fly)
ORGANISM        Drosophila melanogaster
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
                1 (bases 1 to 85518)
REFERENCE       Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
                Burenhoff,C., Champe,M., Chavez,C., Chew,M., Cieciolka,L.,
                Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,L.L.,
                Hoskins,R.A., Houston,K.A., Hummasti,S.R., Kara,K., Kearney,L.,
                Kim,E., Lee,B., Lewis,S., Li,P., Lomoton,M.A., Mazda,P.,
                Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleib,J.M., Park,S.,
                Pfeiffer,B., Poon,L., Punch,E., Sequeira,A., Sethi,H., Snir,E.,
                Switckas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R.,
                Zieran,L.L. and Rubin,G.M.
                Sequencing of Drosophila chromosome 2R, region 44C4-44C5
                2 (bases 1 to 85518)
TITLE           Unpublished (1998)
JOURNAL         JOURNAL
REFERENCE       Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C.,
                Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A.,
                Hummasti,S.R., Kara,K., Kearney,L., Kim,S.H., Lee,B.,
                Lomoton,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R.,
                Moshrefi,M., Nixon,K., Pacleib,J.M., Park,S., Pfeiffer,B., Punch,E.,
                Snir,B., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R.,
                Zieran,L.L. and Kimmel,B.E.
                Direct Submission
                Submitted (14-AUG-1998) Drosophila Genome Center, Lawrence Berkeley
                Laboratory, MS 64-121, Berkeley, CA 94720, USA
                On Dec 23, 1998 this sequence version replaced gi:4049302.
COMMENT         TITLE
                JOURNAL
                REFERENCE
                AUTHORS

```

Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (<http://www.fruitfly.org/sequence/>) or send email
to bdg@fruitfly.berkeley.edu.
Pl library location: 71-45.

FEATURES

source

Location/Qualifiers
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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/map="44C4-44C5"
/clone="P1 DS06765 (D363)"
/clone_1ib="P1 library, partial Sau3A in pAd10sacB11"
BASE COUNT 24282 a 17889 c 18642 g 24705 t
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Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 AACCTTTTACCATATATTA 524

Db 75739 AACCTTTTACCATATATTA 75759

RESULT 15

AL354827/c

LOCUS Human DNA sequence from clone RP11-280J7 on chromosome 13, complete
DEFINITION

ACCESSION AL354827 AC025666

VERSION AL354827.5 GI:12597080

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 127641)

Blakey, S.

Direct Submission

Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

On or before May 15, 2001 this sequence version replaced
gi:17387396, gi:12539586.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone configs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr13>

RP11-280J7 is from the library RPc1-11.1 constructed by the group
of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone
RP11-280J7 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-280J7 is at 127641 in this
sequence. The true right end of clone RP11-475B14 is at 100 in this
sequence.

FEATURES

source

Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 AGTAAATTAAATATATATAA 390

Db 33240 AGTAAATTAAATATATATAA 33220

RESULT 16

AC080184/c

LOCUS Homo sapiens chromosome 13 clone RP11-601J15 map 13, WORKING DRAFT
DEFINITION

ACCESSION AC080184.2 GI:11094827

VERSION AC080184.2 GI:11094827

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 147078)

Birren, B.; Linton, L.; Nusbaum, C. and Lander, E.

Unpublished

2 (bases 1 to 147078)

Birren, B.; Linton, L.; Nusbaum, C.; Lander, E.; Abraham, H.; Allen, N.;
Anderson, S.; Barna, N.; Baetsen, V.; Beda, F.; Boguslavsky, L.;
Bouckgalter, B.; Brown, A.; Burkett, G.; Campiano, A.; Castle, A.;
Choepe, Y.; Colangelo, M.; Collins, S.; Collymore, A.; Cooke, P.;
Dekrellano, K.; Dewar, K.; Diaz, J.S.; Dodge, S.; Ferreira, P.;
Fitzhugh, W.; Gage, D.; Galagan, J.; Gardyna, S.; Ginde, S.; Goyette, M.;
Graham, L.; Grand-Pierre, N.; Hagos, B.; Heatford, A.; Horton, L.;
Iliev, I.; Johnson, R.; Jones, C.; Kann, L.; Karatas, A.; Lacombe, K.;
Lamazeres, R.; Landers, T.; Lehoczy, J.; Levine, R.; Liu, G.;
Macdonald, P.; Marquis, N.; McCarthy, M.; McEwan, P.; McKernan, K.;
McSheehers, R.; Meldrum, J.; Meneses, L.; Mihova, T.; Mlenga, V.;
Morrow, J.; Murphy, T.; Naylor, J.; Norman, C.H.; O'Connor, T.;
O'Donnell, P.; O'Neill, D.; Oliver, R.M.; Oliver, J.; Peterson, K.;
Pierre, N.; Pissani, C.; Pollara, V.; Raymond, C.; Rieback, M.; Riley, R.;
Rogov, P.; Roehman, D.; Roy, A.; Santos, R.; Schauer, S.; Severy, P.;
Sougnier, C.; Spencer, B.; Stange-Thomann, N.; Stojanovic, N.;
Strauss, N.; Subramanian, A.; Talamas, J.; Tesfaye, S.; Theodore, J.;
Tirrell, A.; Travers, M.; Trigglio, J.; Vassiliev, H.; Viel, R.; Vo, A.;
Wilson, B.; Wu, X.; Wyman, D.; Ye, W.-J.; Young, G.; Zainoun, J.;
Zimmer, A. and Zody, M.

Direct Submission

Submitted (28-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147078)

Birren, B.; Linton, L.; Nusbaum, C.; Lander, E.; Abraham, H.; Allen, N.;
Anderson, S.; Barna, N.; Baetsen, V.; Beda, F.; Boguslavsky, L.;
Bouckgalter, B.; Brown, A.; Burkett, G.; Campiano, A.; Castle, A.;
Choepe, Y.; Colangelo, M.; Collins, S.; Collymore, A.; Cooke, P.;
Dekrellano, K.; Dewar, K.; Diaz, J.S.; Dodge, S.; Ferreira, P.;
Fitzhugh, W.; Gage, D.; Galagan, J.; Gardyna, S.; Ginde, S.; Goyette, M.;
Graham, L.; Grand-Pierre, N.; Hagos, B.; Heatford, A.; Horton, L.;
Iliev, I.; Johnson, R.; Jones, C.; Kann, L.; Karatas, A.; Lacombe, K.;
Lamazeres, R.; Landers, T.; Lehoczy, J.; Levine, R.; Liu, G.;
Macdonald, P.; Marquis, N.; McCarthy, M.; McEwan, P.; McKernan, K.;
McSheehers, R.; Meldrum, J.; Meneses, L.; Mihova, T.; Mlenga, V.;
Morrow, J.; Murphy, T.; Naylor, J.; Norman, C.H.; O'Connor, T.;
O'Donnell, P.; O'Neill, D.; Oliver, R.M.; Oliver, J.; Peterson, K.;
Pierre, N.; Pissani, C.; Pollara, V.; Raymond, C.; Rieback, M.; Riley, R.;
Rogov, P.; Roehman, D.; Roy, A.; Santos, R.; Schauer, S.; Severy, P.;
Sougnier, C.; Spencer, B.; Stange-Thomann, N.; Stojanovic, N.;
Strauss, N.; Subramanian, A.; Talamas, J.; Tesfaye, S.; Theodore, J.;
Tirrell, A.; Travers, M.; Trigglio, J.; Vassiliev, H.; Viel, R.; Vo, A.;
Wilson, B.; Wu, X.; Wyman, D.; Ye, W.-J.; Young, G.; Zainoun, J.;
Zimmer, A. and Zody, M.

Direct Submission

Submitted (28-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147078)

Birren, B.; Linton, L.; Nusbaum, C.; Lander, E.; Abraham, H.; Allen, N.;
Anderson, S.; Barna, N.; Baetsen, V.; Beda, F.; Boguslavsky, L.;
Bouckgalter, B.; Brown, A.; Burkett, G.; Campiano, A.; Castle, A.;
Choepe, Y.; Colangelo, M.; Collins, S.; Collymore, A.; Cooke, P.;
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Fitzhugh, W.; Gage, D.; Galagan, J.; Gardyna, S.; Ginde, S.; Goyette, M.;
Graham, L.; Grand-Pierre, N.; Hagos, B.; Heatford, A.; Horton, L.;
Iliev, I.; Johnson, R.; Jones, C.; Kann, L.; Karatas, A.; Lacombe, K.;
Lamazeres, R.; Landers, T.; Lehoczy, J.; Levine, R.; Liu, G.;
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McSheehers, R.; Meldrum, J.; Meneses, L.; Mihova, T.; Mlenga, V.;
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Rogov, P.; Roehman, D.; Roy, A.; Santos, R.; Schauer, S.; Severy, P.;
Sougnier, C.; Spencer, B.; Stange-Thomann, N.; Stojanovic, N.;
Strauss, N.; Subramanian, A.; Talamas, J.; Tesfaye, S.; Theodore, J.;
Tirrell, A.; Travers, M.; Trigglio, J.; Vassiliev, H.; Viel, R.; Vo, A.;
Wilson, B.; Wu, X.; Wyman, D.; Ye, W.-J.; Young, G.; Zainoun, J.;
Zimmer, A. and Zody, M.

Direct Submission

Submitted (28-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 147078)

Birren, B.; Linton, L.; Nusbaum, C.; Lander, E.; Abraham, H.; Allen, N.;
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Bouckgalter, B.; Brown, A.; Burkett, G.; Campiano, A.; Castle, A.;
Choepe, Y.; Colangelo, M.; Collins, S.; Collymore, A.; Cooke, P.;
Dekrellano, K.; Dewar, K.; Diaz, J.S.; Dodge, S.; Ferreira, P.;
Fitzhugh, W.; Gage, D.; Galagan, J.; Gardyna, S.; Ginde, S.; Goyette, M.;
Graham, L.; Grand-Pierre, N.; Hagos, B.; Heatford, A.; Horton, L.;
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Lamazeres, R.; Landers, T.; Lehoczy, J.; Levine, R.; Liu, G.;
Macdonald, P.; Marquis, N.; McCarthy, M.; McEwan, P.; McKernan, K.;
McSheehers, R.; Meldrum, J.; Meneses, L.; Mihova, T.; Mlenga, V.;
Morrow, J.; Murphy, T.; Naylor, J.; Norman, C.H.; O'Connor, T.;
O'Donnell, P.; O'Neill, D.; Oliver, R.M.; Oliver, J.; Peterson, K.;
Pierre, N.; Pissani, C.; Pollara, V.; Raymond, C.; Rieback, M.; Riley, R.;
Rogov, P.; Roehman, D.; Roy, A.; Santos, R.; Schauer, S.; Severy, P.;
Sougnier, C.; Spencer, B.; Stange-Thomann, N.; Stojanovic, N.;
Strauss, N.; Subramanian, A.; Talamas, J.; Tesfaye, S.; Theodore, J.;
Tirrell, A.; Travers, M.; Trigglio, J.; Vassiliev, H.; Viel, R.; Vo, A.;
Wilson, B.; Wu, X.; Wyman, D.; Ye, W.-J.; Young, G.; Zainoun, J.;
Zimmer, A. and Zody, M.

Direct Submission

TITLE
JOURNAL
COMMENT

DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
Fitzhigh,W., Gage,D., Galagan,J., Gardya,S., Ginde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Hearford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Labocque,K.,
Lamazares,R., Landers,T., Lenockzy,J., Levine,R., Liu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McEwan,K.,
McChester,R., Meldrim,J., Menue,L., Mhova,T., Mleaga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rogov,P., Rochman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Sougnaz,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Straus,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
Tirrell,A., Travers,M., Trigglio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.

Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 4, 2000 this sequence version replaced gi:10334904.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: 601_J_15

Center clone name: 111223

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 137099 bases at least Q40
Consensus quality: 142162 bases at least Q30
Consensus quality: 143831 bases at least Q20
Insert size: 172000; agarose-fp
Insert size: 144778; sum-of-contigs
Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 18712: contig of 18712 bp in length
* 18713 18812: gap of 100 bp
* 18813 20419: contig of 1607 bp in length
* 20420 20519: gap of 100 bp
* 20520 21760: contig of 1241 bp in length
* 21761 21860: gap of 100 bp
* 21861 23353: contig of 1493 bp in length
* 23354 23453: gap of 100 bp
* 23454 25619: contig of 2166 bp in length
* 25620 25719: gap of 100 bp
* 25720 27181: contig of 1462 bp in length
* 27182 27281: gap of 100 bp
* 27282 29012: contig of 1731 bp in length
* 29013 29112: gap of 100 bp
* 29113 33172: contig of 4060 bp in length
* 33173 33372: gap of 100 bp
* 33373 37412: contig of 4040 bp in length
* 37413 37412: gap of 100 bp
* 37413 42066: contig of 4654 bp in length
* 42067 42166: gap of 100 bp
* 42167 46649: contig of 4483 bp in length
* 46650 46749: gap of 100 bp

FEATURES	source
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60601	60700: gap of 100 bp
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65227	65326: gap of 100 bp
65327	71626: contig of 6300 bp in length
71627	71726: gap of 100 bp
71727	79581: contig of 7855 bp in length
79582	79681: gap of 100 bp
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90104	90203: gap of 100 bp
90204	98835: contig of 8632 bp in length
98836	98935: gap of 100 bp
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20520. 21760	
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21861. 23353	
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23454. 25619	
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25720. 27181	
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27282. 29012	
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33273. 37312	
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37413. 42066	
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42167. 46649	
/note="assembly_fragment"	
46750. 50665	
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50766. 56271	
/note="assembly_fragment"	
56372. 60600	
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60701. 65226	
/note="assembly_fragment"	
65327. 71626	
/note="assembly_fragment"	
71727. 79581	
/note="assembly_fragment"	
79682. 90103	
/note="assembly_fragment"	
90204. 98835	
/note="assembly_fragment"	
98936. 107000	
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misc_feature /note="assembly_fragment"
107101..117126
/note="assembly_fragment"
misc_feature 117227..129147
/note="assembly_fragment"
misc_feature 129248..146388
/note="assembly_fragment"
misc_feature 146489..147078
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clone_end:T7
vector_side:right"

Query Match 3.4%; Score 21; DB 2; Length 147078;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 AATATTAATCTTTTATTCGCT 299
8923 AATATTAATCTTTTATTCGCT 8903

RESULT 17
AC114263 151802 bp DNA linear INV 12-MAR-2003
DEFINITION Dictyostelium discoideum chromosome 2 map 215673-367476 strain AX4,
complete sequence.
AC114263 AC115602 AC114257 AC114259 AC115589 AC115595
VERSION AC114263.2 GI:28829909
KEYWORDS HTG.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE 1 (bases 1 to 151802)
AUTHORS Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Gulgo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,W.A., Platzer,M., Rosenthal,A. and
Noegel,A.A.
TITLE Sequence and analysis of chromosome 2 of Dictyostelium discoideum
JOURNAL Nature 418 (6893), 79-85 (2002)
MEDLINE 22092622
PUBMED 12097910
REMARK The Dictyostelium Genome Sequencing Consortium
REFERENCE 2 (bases 1 to 151802)
AUTHORS Baumgart,C.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2002) Genome Analysis, Institute of Molecular
Biotechnology, Butenberstr. 11, Jena 07745, Germany
3 (bases 1 to 151802)
REFERENCE 3 (bases 1 to 151802)
AUTHORS Baumgart,C.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Butenberstr. 11, Jena 07745, Germany
4 (bases 1 to 151802)
REFERENCE 4 (bases 1 to 151802)
AUTHORS Baumgart,C.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Butenberstr. 11, Jena 07745, Germany
On or before Mar 4, 2003 this sequence version replaced
gi:19570051, gi:19424353, gi:19352280, gi:19569963, gi:19570010,
gi:19352293.
CDS predictions from Geneid do not necessarily reflect true genes.
Further information is available from IMB Jena, Department of
Genome Analysis
(http://genome.imb-jena.de/dictyostelium/)
and the University Cologne/Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
Funding
Agency : Deutsche Forschungsgemeinschaft (DFG) .
location/Qualifiers
1..151802
/organism="Dictyostelium discoideum"
/mol_type="Genomic DNA"
/strain="AX4"

CDS
/db_xref="taxon:44689"
/map="215673-367476"
join(2001..2126,2360..2622,2773..4673,4767..5044)
/note="Geneid exon scores (in order of location ranges) :
10.75, 20.87, 193.78, 22.94 - GSCJ_ID dd_03029"
/product="similar to Homo sapiens (Human). High-risk human
papilloma viruses E6 oncoproteins targeted protein E6p1
alpha"
/protein_id="AA052401.1"
/db_xref="GI:28829910"
/translation="WDSFQSGLEMLFEVLAEVLPDHPFKOYLSRLTVDKTSI
ILLQPTLKHSFSDVYLNDGKEITEDPQFYTSHRITITLIDQEPKILSKQO
ILLQSNAPAPLSPNSQATISQKQODQNLINIVADLTLSEKSPMVRILSGAPML
IEQHSPTKGKDEKTKYKDRPDLSEKSTNSKLVKVRPKLTKSDSVFPNNNGNITIT
SSPTNSNTTTTTTTTTTTTTTTTTSSSSSSPNSGSPNSGSPKISFLV
NTPOKRRSLSHKQSDLSFSIHGATIRPKTOEQOVLGALESNLNPSNN
NSNNNSGANSNTSSSSTNSRSLIEMIDNNNGGTSISGPFVDYSLIYVSGF
TIESLNNLTPLIVSSGQLEMLNPLTDESPTCKYFGNEHMYTIGDSKRGITVSI
FKESDSQSTASTASSPSPSSSLNLHNSGDQNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NEVVLIRTKNDITRTKIKQFALFGNSRPPYKDIVOGIIIPMCKMILVKNQEI
QKMLKSEERORVSKFGILYICAPGVDESMFCNONGSGFHPLEFIDRLQISG
WKNYRGGLVDKDSNSTGTHSYKQVHSFEIMPHVATLPPNPIDKQOVKKRRLGND
IVLIVKSGDQLPDKYMKSDFNHVFVISIVYVDSKIKYKYSIYKQVSESTPY
LVNSIEMSESEFEFLSKLINSCESSYEAPSFKIKQIRVALDKOMNTYLNPE"
complement(5636..6130)
/note="Geneid exon scores (in order of location ranges) :
32.63 - GSCJ_ID dd_01254"
/codon_start=1
/product="hypothetical protein"
/protein_id="AA052402.1"
/db_xref="GI:28829911"
/translation="MTGNNDNNNNINKISDTLNEKINAFKVLGDHKGFSVLLKTLKL
NKIGYGFIEFVYAKHETWTLDLGAGASATMDGAGFASLYCTQENQKELTFGVY
NMNINVTGATIGDKIIRKQVEKLTTLCTFTVTKIEKADSSLSISQAIIYKPPRF
YSKL"
join(6755..6764,6858..9115)
/note="Geneid exon scores (in order of location ranges) :
-1.56, 152.88 - GSCJ_ID dd_03022"
/codon_start=1
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Hypothetical 231.8 kDa protein"
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/db_xref="GI:28829912"
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NSNNENYEDNEDNDNDNDDNDNDNDINILIGPSGSKSLINSIIYMYRD
SLGALIESNNAIATPTIVSMDSDDNDFNIGIIEDESEKRIVOCKSVYKTK
KYRIKNSIGQSLCPIIDRPGVLDSGIEKDEENPHILNELSKLQKAAVCLIMP
NENRASQVEKFCNELCHLHSAKNIIFPCLSSTSIHTRAGSEYKLAOLIANLU
KERNRIHIEKRTYCEDESFNVLVCKKGGAFSEFELVLSWTSVOELTRLLK
DIISCFHDEKTLINLARTMTNOLIQPTTCVFVNNELKAINERKIEINLNDPL
EIDQLKRLTYTPFNKSLDELDAIYCNLKCISTTEKLVYTDQIKELGVCNCT
NASSGKSVSCSISGLGFCVCSYFTKINIDTIEIRBEIOLPENNDDDDGGGS
NEEGIKLSIKSKEOSRISKDFKSLQDRYOVENELITGSSVOVSEFLCNLSLE
VNEISYIOIILSNKSNCTNGIOSIKLENTGSHKQIIDPKNNLEKQXORDK
QKREKIERGTFYPSQDELONDERNDSEFSVTEIKKINIEIILNKLISGNFISK
LSQFESIKRKYFNPSQIDONDERNDSEFSVTEIKKINIEIILNKLISGNFISK
IFNSFKPNPNKIDIFI"
join(10151..10220,10386..12687,12773..12924,13180..13265)
/note="Geneid exon scores (in order of location ranges) :
5.24, 216.41, 12.62, 3.78 - GSCJ_ID dd_02284"
/codon_start=1
/product="similar to synthetic lethal KAR3; sIk19p
[Schizosaccharomyces cerevisiae]"
/protein_id="AA052404.1"
/db_xref="GI:28829913"
/translation="MKIGSTRFRKTSKLPDAPSPSGIYSNDNSTLNREISTMEPS
LPSSSTSSSTSSSTVSPFTWSIKIIGSQSKSNLSLKQKQWSDPEDIYQLLA
EQCLTQOMTWCGHFDLPFIHQYSIDLINAKENNGSNILISLPASSGEGDPKSKSY
KIAKKLIVAOQINILCKQNVKPRKRWLSTIYGCLINDMLLSYGFQFPSPWLS
LVKQVFTDKIQTDIPLDSCGSEFVDFLLPLKQGGKAKKRIRKDSNLSISQILKO
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[illegible]

```

Query Match
Best Local Similarity    100.0%;   Pred. No. 4.6;
Matches      21; Conservative    0; Mismatches     0; Indels       0; Gaps       0;

OY          370 AGTAAATTATATATATAAAA 390
              |||
Db           1852 AGTAAATTATATATATAAAA 1872
              |||

RESULT 18
LOCUS      AC006017/c                162556 bp      DNA       linear   PRI 21-DEC-1999
DEFINITION Homo sapiens PAC clone RPS-98107 from 7q34-q36, complete sequence.
ACCESSION  AC006017
VERSION     AC006017.2 GI:4508141
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 162556)
AUTHORS     Sulston,P.E. and Waterston,R.
TITLE       Toward a complete human genome sequence
JOURNAL     Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE     99063792
PUBMED      9847074
REFERENCE   2 (bases 1 to 162556)
AUTHORS     Joshua,C. and McCaline,B.
TITLE       The sequence of Homo sapiens PAC clone RPS-98107
JOURNAL     Unpublished
REFERENCE   3 (bases 1 to 162556)
AUTHORS     Waterston,R.H.
TITLE       Direct Submission
JOURNAL     Submitted (22-NOV-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4 (bases 1 to 162556)
AUTHORS     Waterston,R.H.
TITLE       Direct Submission
JOURNAL     Submitted (22-MAR-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5 (bases 1 to 162556)
AUTHORS     Waterston,R.
TITLE       Direct Submission
JOURNAL     Submitted (28-JUL-1999) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   6 (bases 1 to 162556)
AUTHORS     Waterston,R.
TITLE       Direct Submission
JOURNAL     Submitted (21-DEC-1999) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
            On Mar 24, 1999 this sequence version replaced gi:3907501.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@watscn.wustl.edu
----- Summary Statistics -----
Center project name: H_DD0981007
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
```

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCL-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong. VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP4-66917. Actual start of this clone is at base position 1 of RP5-98107; actual end is at 162556 of RP5-98107.

The run of A's from 125217 to 125241 may contain one less A, no read was able to make an exact call.

FEATURES

source Location/Qualifiers

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1..162556
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"
  /chromosome="7"
  /map="7q34-q36"
  /clone="RP5-98107"
  /clone_1fb="RPCL-5"
  8..202
    /rpt_family="L2"
    repeat_region
    668..750
      /rpt_family="L2"
      repeat_region
    760..1053
      /rpt_family="Alu"
      repeat_region
    1131..1425
      /rpt_family="Alu"
      repeat_region
    1575..1748
      /rpt_family="MIR"
      repeat_region
    2524..2623
      /rpt_family="MaLR"
      repeat_region
    2791..2852
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      repeat_region
    2915..2984
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      repeat_region
    2991..3022
      /rpt_family="L1"
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    3023..3051
      /rpt_family="CAAAn"
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    3052..3327
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    3328..3599
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    4044..4128
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    4300..4321
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      repeat_region
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  /rpt_family="MIR"
  repeat_region 4920..5210
    /rpt_family="Alu"
    misc_feature 5286..5436
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    gene <5287..10444
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      /note="WUGSC:H_DJ0981007.1"
      /note="similar to glycosyl transferases; similar to CAA22098 (PID:g3980030); H_DJ0981007.1"
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      /evidence=not experimental
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      /db_xref="GI:5630078"
      /transcript="TMCQGLFTIPCSRGHISKQTKPSTISANTHNYLRVH
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      5535..5711
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        repeat_region 6004..6301
          /rpt_family="Alu"
          repeat_region 6341..6386
            /rpt_family="MER1_type"
            repeat_region 6663..6766
              /rpt_family="L1"
              repeat_region 6767..7063
                /rpt_family="Alu"
                repeat_region 7064..7395
                  /rpt_family="L1"
                  repeat_region 7396..7709
                    /rpt_family="Alu"
                    repeat_region 7710..7729
                      /rpt_family="L1"
                      repeat_region 7730..8077
                        /rpt_family="MER2_type"
                        repeat_region 8078..8202
                          /rpt_family="L1"
                          repeat_region 8357..8483
                            /rpt_family="L1"
                            repeat_region 8484..8786
                              /rpt_family="Alu"
                              repeat_region 8787..9101
                                /rpt_family="L1"
                                repeat_region 9817..9905
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                                  misc_feature 10284..10499
                                    /note="match to EST AA907643 (NID:g3043103) om30c11.s1"
                                    misc_feature 10289..10485
                                      /note="match to EST AI150152 (NID:g3678621) qf44h12.x1"
                                      repeat_region 11036..11308
                                        /rpt_family="Alu"
                                        repeat_region 11673..11730
                                          /rpt_family="L2"
                                          repeat_region 11731..12032
                                            /rpt_family="Alu"
                                            repeat_region 12279..12291
                                              /rpt_family="Alu"
                                              repeat_region 12292..12595
                                                /rpt_family="Alu"
                                                repeat_region 12596..12771
                                                  /rpt_family="Alu"
                                                  repeat_region 12870..12924
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                                                    repeat_region 13449..13583
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                                                      repeat_region 13610..13693
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Query Match 3.4%; Score 21; DB 9; Length 162556;
Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 234 TTTATTATTATTGCTCA 254
 |||||
 Db 44465 TTTATTATTATTGCTCA 44445

RESULT 19
 AL646050 164018 bp DNA linear ROD 14-MAR-2002
 LOCUS Mouse DNA sequence from clone RP23-460G5 on chromosome 11, complete
 DEFINITION
 ACCESSION AL646050
 VERSION AL646050
 KEYWORDS HTG.
 SOURCE HTG.
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 164018)
 TITLE Direct Submission
 JOURNAL Submitted (14-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk; Clone requests: clonerequests@sanger.ac.uk
 On Mar 21, 2002 this sequence version replaced gi:19309548.

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-460G5 is from the RP23-Mouse PAC library

constructed by the group of Pieter de Jong.
 For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: DBAC3.6
 IMPORTANT: This sequence is not the entire insert of clone RP23-460G5. It may be shorter because we sequence overlapping sections only once, except for a short overlap.
 The true right end of clone RP23-460G5 is at 164018 in this sequence. The true right end of clone RP23-298113 is at 2000 in this sequence.

FEATURES

source
 1. 164018
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
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 /clone_1id="RP23-23"
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 /clone_1id="RP23-23"
 /note="Sequence confirmed by mouse whole genome shotgun sequencing data, sequenced by the Mouse Genome Sequencing Consortium, contig 126003215, version 1."

misc_feature
 63783..63798
 /note="Sequence confirmed by mouse whole genome shotgun sequencing data, sequenced by the Mouse Genome Sequencing Consortium, contig 126003215, version 1."

BASE COUNT 50254 a 31520 c 32168 g 50076 t

ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 164018;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 234 TTTATTATTATTGCTCA 254
 |||||
 Db 9573 TTTATTATTATTGCTCA 9593

RESULT 20
 AC021838 166438 bp DNA linear HTG 04-APR-2000
 LOCUS Homo sapiens chromosome 6 clone RP11-4L15 map 6, WORKING DRAFT
 DEFINITION
 ACCESSION AC021838
 VERSION AC021838.3
 KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
 SOURCE HTG.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 166438)
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-2000) Whitehead Institute/MIT Center for Genome Research
 Research, 320 Charles Street, Cambridge, MA 02144, USA
 On Apr 4, 2000 this sequence version replaced gi:16984455.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

COMMENT

Direct Submission
 Submitted (20-UN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02144, USA
 On Apr 4, 2000 this sequence version replaced gi:16984455.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE

JOURNAL

Center: Whitehead Institute/MIT Center for Genome Research
 Center code: WIRB
 Web site: <http://www.seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L6010
 Center clone name: 4_L_15

----- Summary Statistics
 Sequencing Vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 159804 bases at least Q40
 Consensus quality: 162919 bases at least Q30
 Consensus quality: 164262 bases at least Q20
 Insert size: 167000; agarose-fp
 Insert size: 165238; sum-of-ctg
 Quality coverage: 4.5 in Q20 bases; agarose-fp
 Quality coverage: 4.5 in Q20 bases; sum-of-ctg

----- NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will

```

* be preserved.
1 1110: contig of 1110 bp in length
* 1111 1210: gap of 100 bp
* 1211 2074: contig of 864 bp in length
* 2075 2174: gap of 100 bp
* 2175 4720: contig of 2546 bp in length
* 4721 4820: gap of 100 bp
* 4821 8287: contig of 3467 bp in length
* 8288 8387: gap of 100 bp
* 8388 13431: contig of 5044 bp in length
* 13432 13531: gap of 100 bp
* 13532 21554: contig of 8023 bp in length
* 21555 34613: contig of 12959 bp in length
* 34614 34713: gap of 100 bp
* 34714 46970: contig of 12257 bp in length
* 46971 62608: gap of 100 bp
* 62609 62708: gap of 100 bp
* 62709 78889: contig of 16180 bp in length
* 78890 103384: gap of 100 bp
* 103385 103484: gap of 100 bp
* 103485 134361: contig of 30877 bp in length
* 134362 134461: gap of 100 bp
* 134462 166438: contig of 31977 bp in length.
FEATURES
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/map="6"
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/clone_lib="RPCT-11 Human Male BAC"
1. 1110
/note="assembly_fragment"
misc_feature
1211. 2074
/note="assembly_fragment"
clone_end:sp6
vector_side:right"
2175. 4720
/note="assembly_fragment"
misc_feature
4821. 8287
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8388. 13431
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21655. 34613
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34714. 46970
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misc_feature
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vector_side:right"

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BASE COUNT 49284 a 32025 c 31847 g 52054 t 1228 others
ORIGIN

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Query Match 3.4%; Score 21; DB 2; Length 166438;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
272 TGATGCCAATATCTTTTA 292

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Db 156305 TGATGCCAATATCTTTTA 156325

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RESULT 21
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LOCUS
DEFINITION
AC008187 168417 bp DNA linear INV 10-MAR-2001
Drosophila melanogaster, chromosome 2R, region 47D-47E, BAC clone
BAC13D20, complete sequence.
AC008187
AC008187 GI:13270533
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 168417)
REFERENCE
AUTHORS
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, J., An, H., Baldwin, D., Bantz, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Chao, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Dou, L.E., Doyle, C., Dresnek, D., Fartan, D.,
Ferreira, S., Frisoe, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegan, C., Jalali, M., Kruse, D., Li, P., Matzel, B., Moshirefi, A.,
McIntosh, I.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pachet, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phuanaenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskaas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Sequencing of Drosophila chromosome 2R, region 47D-47E
Unpublished
2 (bases 1 to 168417)

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TITLE
JOURNAL
REFERENCE
AUTHORS
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Fartan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummel, S.R., Katta, K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomoth, M.A., Mazda, P.,
Moshirefi, A.R., Moshirefi, M., Nixon, K., Pachet, J.M., Park, S.,
Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snit, E.,
Svirskaas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
Rubin, G.M.
Direct Submission
Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Mar 10, 2001 this sequence version replaced gi:7259657.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720

```

```

COMMENT
This sequence was assembled using end sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to hdg@fruitfly.berkeley.edu.
Location/Qualifiers
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Drosophila melanogaster BAC library, partial EcoRI in
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FEATURES
source

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ORIGIN

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Query Match 3.4%; Score 21; DB 3; Length 168417;

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Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

	RESULT	22
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LOCUS		
DEFINITION	Mus musculus clone RP24-16UJ12, WORKING DRAFT SEQUENCE, 5 ordered	
	174595 bp	DNA linear HTG 21-OCT-2007
AC114655		

ACCESSION AC114655
VERSION 4
KEYWORDS GI:24182179
SOURCE HTG, HTGS_PHASE2, HTGS_DRAFT, HTGS_FULLTOP
ORGANISM Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
TITLE

Mus musculus, clone RP24-160J12
Birren, B., Nusbaum, C. and Lander, E.
1 (bases 1 to 174595)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mus musculus, clone RP24-160J12

JOURNAL REFERENCE AUTHORS	Unpublished 2 (bases 1 to 174595) Birren, B., Linton, L., Nusbaum, C., I
---------------------------------	--

AUTHORS
 Birren, B., Jinton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barua, N., Bastien, V., Bloom, T., Bogutsky, L.,
 Boukhalter, B., Brown, A., Camarata, J., Campolano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, W., Collins, S., Collamore, A.,
 Cook, A., Cooke, P., DeRellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fato, S., Ferreira, P., Fitzgung, W., Gage, D., Galagan, J., Gardyna, S.,
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 Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
 Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Ribbeck, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Stenga-Thomann, N., Stojanovic, N.,
 Straus, N., Subramanian, A., Talamas, J., Teyfay, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zemek, L., Zimmer, A. and Zody, W.

TITLE Direct Submission
JOURNAL Submitted (10-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 174595)

AITIKHOKS
 Britten, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
 Barrin, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhigbo, A.,
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, C., Diaz, J. S., Dodge, S.,
 Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Gabaian, J.,
 Gargya, S., Gord, S., Graham, L., Grand-pierre, N., Hafez, N.,
 Haggos, B., Horton, L., Hulme, W., Illiev, I., Johnson, R., Jones, C.,
 Kemat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
 Lindahl-Ton, K., Liu, S., Maclean, C., Macdonald, P., Major, T.,
 Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Minova, T.,
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, C., Oliver, J.,
 Peterson, K., Phunhthang, P., Pierre, N., Raymond, C., Retta, R.,
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 Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K.,
 Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission

JOURNAL Submitted (21-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Oct 21, 2002 this sequence version replaced gi:21362165.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center

Center/Whitehead Institute/ MIT Center for Genome Research
 Center code: MIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information

```
Center project name: L24414
Center clone name: 160_J_12
----- Summary Statistics -----
```

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly: none; 0.00071

Assembly program: Philap; Version 0.960/31
Consensus quality: 172913 bases at least Q40
Consensus quality: 173845 bases at least Q30

Consensus quality: 174088 bases at least Q20
Insert size: 163000; agarose-fp

Insert size: 174195; sum-of-contigs
Quality coverage: 12.6 in Q20 bases; agarose-fp

Quality coverage: 11.8 in Q20 bases; sum-of-cont

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pre-

* of the gaps between them are based on estimates provided by the submitter.
* This sequence will be replaced

- * by the finished sequence as soon as it is available
- * the accession number will be preserved.

* 1 4975: contig of 4975 bp in length
 * 4976 5075: gap of 100 bp

5076	30329: contig of 25254 bp in length
30330	30429: gap of 100 bp

Accession	Contig	Length
30430	70338: contig of 39909 bp in length	39909
70339	70438: gap of 100 bp	100
70430	70438: gap of 100 bp	100

*	70439	121125: concig of 5068 bp in length
*	121126	121225: gap of 100 bp
*	121226	174595: concig of 53370 bp in length

Location/Qualifiers
1.0.174595

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52469 a 34874 c 34404 g 52448 t 400 others

3.4%; Score 21; DB 2; Length 17459

1 Similarly 100.0%; Freq. NO. 4.0;
21; Conservative 0; Mismatches 0; Indels

26 GTATATGCTTATTATTAT 246

83 GTATATGCTTATTATTAT 87063

AL831725	174712 bp	DNA	linear
----------	-----------	-----	--------

DEFINITION Mouse DNA sequence from clone RP23-106P7 on chromosome X, complete sequence.

ACCESSION AL831725

VERSION AL831725.5 GI:22798440

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 174712)

AUTHORS Heath, P.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

COMMENT On Sep 12, 2002 this sequence version replaced gi:22416161.

----- Genome Center -----

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-106P7 is from the RPI-23 Mouse PAC library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

FEATURES

source 1..174712

Location/Qualifiers

/organism="Mus musculus"

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/db_xref="taxon:10090"

/chromosome="X"

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BASE COUNT 52726 a 34512 c 35016 g 52458 t

ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 174712;

Best Local Similarity 100.0%; Pred. NO. 4.6;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 ATGGAGTAATTATATATAT 386

Db 91785 ATGGAGTAATTATATATAT 91765

RESULT 24

AC110071 174902 bp. DNA linear HTG 09-FEB-2002

LOCUS Homo sapiens chromosome UNK clone RPI3-875011, WORKING DRAFT

AC110071 SEQUENCE, 12 unordered pieces.

ACCESSION AC110071.1 GI:18642891

VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 174902)

AUTHORS Waterston, R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 174902)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (09-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Contact: submissions@wustl.edu

----- Project Information -----

Center project name: H_FH0875011

Summary Statistics -----

Sequencing vector: M13; 2%

Sequencing vector: Plasmid; 98%

Chemistry: Dye-primer ET; 0% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 171309 bases at least Q40

Consensus quality: 172330 bases at least Q30

Consensus quality: 172787 bases at least Q20

Insert size: 197000; agarose-fp

Insert size: 175023; sum-of-contigs

Quality coverage: 7.55 in Q20 bases; agarose-fp

Quality coverage: 6.37 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1114: contig of 1114 bp in length

1115 1214: gap of unknown length

1215 2396: contig of 1182 bp in length

2397 2496: gap of unknown length

2497 3597: contig of 1101 bp in length

3598 3697: gap of unknown length

3698 6579: contig of 2882 bp in length

6580 6679: gap of unknown length

6680 8469: contig of 1790 bp in length

8470 8569: gap of unknown length

8570 11032: contig of 2463 bp in length

11033 11132: gap of unknown length

11133 15590: contig of 4458 bp in length

15591 15690: gap of unknown length

15691 27937: contig of 12247 bp in length

27938 28037: gap of unknown length

28038 47310: contig of 19273 bp in length

47311 47411: gap of unknown length

47412 68421: contig of 21011 bp in length

68422 68521: gap of unknown length

68522 119833: contig of 51312 bp in length

119834 119933: gap of unknown length

119934 174902: contig of 54969 bp in length.

Location/Qualifiers

1..174902

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/mol_type="genomic DNA"

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FEATURES

source

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156734. .158600
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199667. .201534
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misc_feature      /note="assembly_name:Contig17
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Query	3.4%; Score 21; DB 2; Best Local Similarity 100.0%; Matches 21; Conservative 0;	Length 174902; Pred. No. 4.6; Mismatches 0; Indels 0; Gaps 0;
234 TTTATTTATTTATGTTGCTCA	254	
Db 168010 TTTATTTATTTATGTTGCTCA	168030	

RESULT	25
AC117760/c	
LOCUS	AC117760 191470 bp DNA linear HTG 11-MAR-2003
DEFINITION	Mus musculus clone RP24-421O23, WORKING DRAFT SEQUENCE, 11 unorderd pieces.
ACCESSION	AC117760
VERSION	AC117760.3 GI:28913296
KEYWORDS	HTG; MUSCS PHASE1; HTGS_DRAFT.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 191470)
TITLE	Britten,B., Nusbaum,C. and Lander,E.
JOURNAL	Mus musculus, clone RP24-421O23
AUTHORS	Unpublished 2 (bases 1 to 191470) Britten,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Batza,N., Bastien,V., Bloom,T., Boguski,J., Boukhalter,B., Brown,A., Camarero,J., Campiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A., Cooke,P., DeRellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., Fitzmugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Ilev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., MacDonald,P., Major,O., Margulis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Menkus,L., Mihova,T., Menga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Nobuoka,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnuppck,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stefanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

TITLE	Direct Submission
JOURNAL	Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Mar 11, 2003 this sequence version replaced gi 28354950.

TITLE Direct Submission
JOURNAL Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 191470)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N.,

Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G.,
Zainoun, J., Zembock, L., Zimmer, A. and Zody, W.

Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 191470)

Birren, B., Nusbaum, C., Lander, E., Abouelelli, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Bouckigalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collimore, A., Cook, A., Cooke, P., Corum, B., Deaellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erikson, J., Faro, S.,
Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamet, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C.,
Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M.,
McElrath, J., Meneses, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhara, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Reita, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, R.,
Talmage, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkatesaman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembock, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 11, 2003 this sequence version replaced gti:28394940.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

```

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence\_submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L25649
Center clone name: 421.O.23
-----
Summary Statistics
Sequencing vector: Plasmid, n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 188558 bases at least Q40
Consensus quality: 189590 bases at least Q30
Consensus quality: 189992 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 190470; sum-of-ctigs
Quality coverage: 7.8 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-ctigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1
52533: contig of 52533 bp in length
52534 52533: gap of 100 bp
52634 53750: contig of 1117 bp in length
53751 53850: gap of 100 bp
53851 57435: contig of 3585 bp in length
57436 57535: gap of 100 bp
57536 61130: contig of 3595 bp in length
61131 61230: gap of 100 bp
61231 68870: contig of 7640 bp in length
68871 68970: gap of 100 bp
68971 74009: contig of 5039 bp in length

```



```

*      74010      74109: gap of 100 bp
*      74110      83473: contig of 9364 bp in length
*      83474      83573: gap of 100 bp
*      83574      107469: contig of 23896 bp in length
*      107470      107569: gap of 100 bp
*      107570      136038: contig of 28467 bp in length
*      136037      136136: gap of 100 bp
*      136137      179386: contig of 43250 bp in length
*      179387      179487: gap of 100 bp
*      179487      191470: contig of 11984 bp in length.

```

FEATURES

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source
1..191470
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-421023"
/clone_1lb="RPCT-24 Male Mouse BAC"
1..52533
/misc_feature
/clone="assembly_fragment"
/clone_end:SP6
vector_side:left"
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/misc_feature
/clone="assembly_fragment"
53851..57435
/misc_feature
/clone="assembly_fragment"
57536..61130
/misc_feature
/clone="assembly_fragment"
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/misc_feature
/clone="assembly_fragment"
68971..74009
/misc_feature
/clone="assembly_fragment"
74110..83473
/misc_feature
/clone="assembly_fragment"
83574..107469
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/clone="assembly_fragment"
107570..136038
/misc_feature
/clone="assembly_fragment"
136137..179386
/misc_feature
/clone="assembly_fragment"
179487..191470
/misc_feature
/clone="assembly_fragment"
vector_end:R7

```

```

BASE COUNT      56044 a 41540 c 39948 g 52931 t 1007 others
ORIGIN

```

```

Query Match      3.4%; Score 21; DB 2; Length 191470;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      279 AATATTACTTTTATGCTGT 299
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Db      76814 AATATTACTTTTATGCTGT 76794

```

```

RESULT 26
AC127272      193156 bp      DNA      linear      HTG 31-MAY-2003
LOCUS
DEFINITION Mus musculus chromosome UNK clone RP24-63G5, WORKING DRAFT
AC127272
SEQUENCE, 4 unordered pieces.
AC127272.3 GI:31249905
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 193156)
AUTHORS Wilson,R.K.
TITLE The sequence of Mus musculus clone,
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 193156)
AUTHORS McPherson,J.D. and Waterston,R.H.

```

```

TITLE Direct Submission
JOURNAL Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 193156)
AUTHORS Wilson,R.K.
JOURNAL Direct Submission
Submitted (31-MAY-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On May 31, 2003 this sequence version replaced gi:22203935.

```

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
----- Project Information -----
Center project name: M_BB063G05

```

----- Summary Statistics -----

```

Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 192338 bases at least Q40
Consensus quality: 192489 bases at least Q30
Consensus quality: 192624 bases at least Q20

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

*      1      3283: contig of 3283 bp in length
*      3284      3384: gap of unknown length
*      3384      10348: contig of 6965 bp in length
*      10349      10448: gap of unknown length
*      10449      20538: contig of 10090 bp in length
*      20539      20638: gap of unknown length
*      20639      193156: contig of 172518 bp in length.

```

FEATURES

```

source
1..193156
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP24-63G5"
1..3283
/misc_feature
/clone="assembly_name:Contig2"
3384..10348
/misc_feature
/clone="assembly_name:Contig3"
10449..20538
/misc_feature
/clone="assembly_name:Contig4"
20639..193156
/misc_feature
/clone="assembly_name:Contig5"

```

```

BASE COUNT      57714 a 36287 c 36527 g 62327 t 301 others
ORIGIN

```

```

Query Match      3.4%; Score 21; DB 2; Length 193156;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      528 AAGTCCTTCAGGTGTGCAGG 548
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Db      107186 AAGTCCTTCAGGTGTGCAGG 107206

```

```

RESULT 27
AC073853      193157 bp      DNA      linear      HTG 17-AUG-2000
LOCUS

```


DEFINITION Homo sapiens chromosome 6 clone RP11-763L6, WORKING DRAFT SEQUENCE.
33 unordered pieces.

ACCESSION AC073853
VERSION AC073853.2 GI:9838342
KEYWORDS HMG, HMGs_PHASE1, HMGs_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 193157)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 193157)
Waterston, R.H.
Direct Submission
Submitted (29-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:8810552.

COMMENT ----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
----- Project Information -----
Project name: H NH0763L06
----- Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: Plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 170587 bases at least Q40
Consensus quality: 178667 bases at least Q30
Consensus quality: 182600 bases at least Q20
Insert size: 206000; agarose-fp
Insert size: 190166; sum-of-contigs
Quality coverage: 3.06 in Q20 bases; agarose-fp
Quality coverage: 3.39 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1452: contig of 1452 bp in length
* 1453 1552: gap of unknown length
* 1553 3244: contig of 1692 bp in length
* 3245 3344: gap of unknown length
* 3345 4734: contig of 1390 bp in length
* 4735 4834: gap of unknown length
* 4835 6349: contig of 1515 bp in length
* 6350 6449: gap of unknown length
* 6450 8132: contig of 1683 bp in length
* 8133 8232: gap of unknown length
* 8233 10016: contig of 1784 bp in length
* 10017 10116: gap of unknown length
* 10117 12142: contig of 2026 bp in length
* 12143 12342: gap of unknown length
* 12343 13838: contig of 1686 bp in length
* 13839 14038: gap of unknown length
* 14039 15728: contig of 1690 bp in length
* 15729 15828: gap of unknown length
* 15829 18108: contig of 2280 bp in length
* 18109 18208: gap of unknown length
* 18209 21376: contig of 3168 bp in length
* 21377 21476: gap of unknown length
* 21477 24103: contig of 2627 bp in length
* 24104 24203: gap of unknown length

FEATURES	source
misc_feature	24204 27825: contig of 3622 bp in length
misc_feature	27826 27925: gap of unknown length
misc_feature	27926 31332: contig of 3407 bp in length
misc_feature	31333 31432: gap of unknown length
misc_feature	31433 36077: contig of 4645 bp in length
misc_feature	36078 36177: gap of unknown length
misc_feature	36178 40497: contig of 4320 bp in length
misc_feature	40498 40597: gap of unknown length
misc_feature	40598 45214: contig of 4617 bp in length
misc_feature	45215 45315: gap of unknown length
misc_feature	45316 50376: contig of 5062 bp in length
misc_feature	50377 50477: gap of unknown length
misc_feature	50478 56846: contig of 6370 bp in length
misc_feature	56847 63713: contig of 6767 bp in length
misc_feature	63714 63813: gap of unknown length
misc_feature	63814 70453: contig of 6640 bp in length
misc_feature	70454 77281: contig of 6728 bp in length
misc_feature	77282 77382: gap of unknown length
misc_feature	77383 84766: contig of 7385 bp in length
misc_feature	84767 84865: gap of unknown length
misc_feature	84866 91565: contig of 6699 bp in length
misc_feature	91566 91665: gap of unknown length
misc_feature	91666 99088: contig of 7423 bp in length
misc_feature	99089 108098: gap of unknown length
misc_feature	108099 108198: contig of 8910 bp in length
misc_feature	108199 114947: gap of unknown length
misc_feature	114948 115047: contig of 6749 bp in length
misc_feature	115048 126524: contig of 11477 bp in length
misc_feature	126525 138219: gap of unknown length
misc_feature	138220 138319: contig of 11595 bp in length
misc_feature	138320 152121: gap of unknown length
misc_feature	152122 152221: contig of 13802 bp in length
misc_feature	152222 165974: gap of unknown length
misc_feature	165975 166074: contig of 13753 bp in length
misc_feature	166075 179999: gap of unknown length
misc_feature	180000 180099: contig of 13925 bp in length
misc_feature	180100 193157: gap of unknown length
misc_feature	193158 193157: contig of 13058 bp in length.
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misc_feature	/mol_type="genomic DNA"
misc_feature	/db_xref="taxon:9606"
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misc_feature	1553. 3244
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misc_feature	3345. 4734
misc_feature	/note="assembly_name:Contig14"
misc_feature	4835. 6349
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misc_feature	8233. 10016
misc_feature	/note="assembly_name:Contig17"
misc_feature	10117. 12142
misc_feature	/note="assembly_name:Contig18"
misc_feature	12243. 13938
misc_feature	/note="assembly_name:Contig19"
misc_feature	14039. 15728
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misc_feature	15829. 18108
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misc_feature	18209. 21376
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misc_feature	21477. 24103
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misc_feature	24204. 27825

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31433..336077
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36178..40497
misc_feature /note="assembly_name:Contig27"
40598..45214
misc_feature /note="assembly_name:Contig28"
45315..50376
misc_feature /note="assembly_name:Contig29"
50477..56846
misc_feature /note="assembly_name:Contig30"
56947..63713
misc_feature /note="assembly_name:Contig31"
63814..70453
misc_feature /note="assembly_name:Contig32"
70554..77281
misc_feature /note="assembly_name:Contig33"
77382..84766
misc_feature /note="assembly_name:Contig34"
84867..91565
misc_feature /note="assembly_name:Contig35"
91666..99088
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108199..114947
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115048..126524
misc_feature /note="assembly_name:Contig39"
126625..138219
misc_feature /note="assembly_name:Contig40"
138320..152121
misc_feature /note="assembly_name:Contig41"
clone_end:177
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/note="assembly_name:Contig42"
166075..179999
misc_feature /note="assembly_name:Contig43"
clone_end:SP6
vector_side:left"
misc_feature 180100..193157
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BASE COUNT 57340 a 37593 c 37870 g 57114 t 3240 others
ORIGIN

Query Match 3.4%; Score 21; DB 2; Length 193157;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 TGATGCATATTTACTTTT 292
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DB 140189 TGATGCATATTTACTTTT 140209

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RESULT 28
AC091388 194036 bp DNA linear INV 19-APR-2001
DEFINITION Drosophila melanogaster, chromosome 2R, region 44C-44D, BAC clone
AC091388
AC091388 complete sequence.
AC091388.1 GI:13676915
HTG.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 194036)
Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,

```

Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Fartan,D.,
Ferreira,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phoumanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Swirekas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
Sequencing of Drosophila chromosome 2R, region 44C-44D
Unpublished
2 (bases 1 to 194036)
Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Fartan,D.,
Ferreira,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
Phoumanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Swirekas,R., Tector,C., Williams,S.M.,
Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
Direct Submission
Submitted (19-APR-2001) Berkeley Drosophila Genome Project, MS
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu.
Location/Qualifiers
FEATURES
source
1..194036
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
/map="44C-44D"
/clone="BACR14B02 (D1257)"
/clone_lib="RP11-98 (Roswell) Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
PBACs3.6)"
BASE COUNT 54625 a 42536 c 42389 g 54486 t
ORIGIN

Query Match 3.4%; Score 21; DB 3; Length 194036;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 AAATTTTACATTAATTA 524
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DB 75645 AAATTTTACATTAATTA 75665

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RESULT 29
AC009120 195342 bp DNA linear PRI 28-FEB-2001
DEFINITION Homo sapiens chromosome 16 clone RP11-484B3, complete sequence.
AC009120
AC009120.8 GI:13162505
HTG.
Homo sapiens (human)

ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumakarya; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 195342)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 195342)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 195342)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Feb 28, 2001 this sequence version replaced gi:19256141.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.6.
STS Content:
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/db_xref="taxon:9606"
/chromosome="16"
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BASE COUNT 60656 a 41071 c 39465 g 54150 t
ORIGIN
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 279 AATATTACTTTTATTGCTGT 299
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RESULT 30
AC109217/c 195514 bp DNA linear HTG 06-JUN-2003
LOCUS Mus musculus clone RP23-406P18, *** SEQUENCING IN PROGRESS ***, 2
DEFINITION Ordered pieces.
AC109217
AC109217.6 GI:31442466
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEPIN.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 195514)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP23-406P18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 195514)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R.,
Landers, T., Lehocsky, J., Levine, R., Liu, G., Maclean, C.,
Macedonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,

McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mhova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunhangan, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Riedack, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vasilev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M.J., Young, G.,
Zainoun, U., Zemek, L., Zimmer, A. and Zody, M.
Direct Submission
JOURNAL Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 195514)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelkell, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Chapel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., Dearrellano, K.,
Diaz, J.S., Dodge, S., Doolley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafiz, N., Hagopian, D., Hagos, B.,
Hall, U., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Liu, A., Mabbitt, R., Maclean, C.,
Macedonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrum, J., Meneus, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunhangan, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vasilev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, U., Zemek, L., Zimmer, A. and Zody, M.
Direct Submission
JOURNAL Submitted (06-JUN-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 6, 2003 this sequence version replaced gi:3094997.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L20689
Center clone name: 406_P_18

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 45237: contig of 45237 bp in length
* 45238 45337: gap of 100 bp
* 45338 195514: contig of 15017 bp in length.

FEATURES
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/clone.lib="RP23-406P18"
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 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 528 AACGCTTACAGTGTGCAGA 548
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 Db 23203 AAGTCCTTACAGTGTGCAGA 23183

RESULT 31
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 LOCUS Homo sapiens Xp BAC RP11-339516 (Rosewell Park Cancer Institute
 DEFINITION Human BAC Library) complete sequence.
 AC078957
 VERSION AC078957.16 GI:12600444
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooke, S.L., Amaratunga, H.C., Are, J.R., Banks, T., Barbarta, J., Benton, U., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowles, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buha, C., Burch, P., Burrell, C., Burrell, K.L., Byrd, N.C., Carion, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hayes, A., Hernandez, U., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homs, J., Howard, S., Huber, J., Hulvik, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudish, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovar, J., Kovar, C., Kratovic, J., Kuresli, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsseg, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Meier, Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokemkwo, S., Ogun, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojupokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shooshari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Suton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleceyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D. and Gibbs, R.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 198088)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (13-ATG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 198088)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (01-JAN-2001) Human Genome Sequencing Center, Department

REFERENCE
 AUTHORS of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 TITLE Direct Submission
 JOURNAL Submitted (07-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (29-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
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REFERENCE
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 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

REFERENCE
 AUTHORS Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 198088)
 Worley, K.C.

FEATURES

source

1. 198088

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="X"

/clone="RP11-339516"

/note="overlaps bases 1..2007 of clone AC096506"

/function="clone overlap"

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/rpt_family="LTR33A"

QUALSTAT-REPORT

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Mnc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

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                    /rpt_family="(TTA)n"
repeat_region      complement(2344..2629)
                    /rpt_family="AluSc"
repeat_region      2630..2651
                    /rpt_family="(TTA)n"
repeat_region      4247..4277
                    /rpt_family="(T)n"
repeat_region      complement(5308..5440)
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repeat_region      complement(6105..6332)
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repeat_region      complement(6333..6645)
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repeat_region      complement(6646..6723)
                    /rpt_family="L2"
repeat_region      complement(6724..7111)
                    /rpt_family="THE1C"
repeat_region      complement(7112..8639)
                    /rpt_family="THE1C-internal"
repeat_region      complement(8640..8746)
                    /rpt_family="AluO"
repeat_region      complement(8753..8877)
                    /rpt_family="L2"
repeat_region      complement(8904..9084)
                    /rpt_family="L1MD2"
repeat_region      complement(9083..9415)
                    /rpt_family="L1MD2"
repeat_region      complement(9435..9900)
                    /rpt_family="L2"
repeat_region      9956..10227
                    /rpt_family="AluSp"
repeat_region      complement(10636..10797)
                    /rpt_family="L1PA8"
repeat_region      10840..10934
                    /rpt_family="MIR"
repeat_region      complement(11224..11439)
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repeat_region      12288..12608
                    /rpt_family="AluSc"
repeat_region      12745..12819
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repeat_region      complement(12844..13001)
                    /rpt_family="MER5A"
repeat_region      complement(13579..14024)
                    /rpt_family="MER110A"
repeat_region      14277..14370
                    /rpt_family="MER5A"
repeat_region      complement(14434..14566)
                    /rpt_family="FLAM_A"
repeat_region      complement(14593..14762)
                    /rpt_family="MIR"
repeat_region      16144..16186
                    /rpt_family="(TG)n"
repeat_region      complement(16425..16716)
                    /rpt_family="AluSc"
repeat_region      16801..16844
                    /rpt_family="(TG)n"
repeat_region      complement(16983..17079)
                    /rpt_family="L2"
repeat_region      17737..17757

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Query Match 3.4%; Score 21; DB 9; Length 196088;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 372 TAAATTTAATTAATAAGG 392
 DB 183404 TAAATTTAATTAATAAGG 183424

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RESULT 32
AC126275
LOCUS 215435 bp DNA linear HTG 04-JUL-2002
DEFINITION Mus musculus chromosome UNK clone RP23-11N117, WORKING DRAFT
ACCESSION AC126275
VERSION AC126275.1 GI:21694003
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 215435)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
2 (bases 1 to 215435)
McPherson,J.D. and Waterston,R.H.
Direct Submission
Submitted (04-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

```

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA011N17
-----

```

----- Summary Statistics -----

```

Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 209748 bases at least Q40
Consensus quality: 210894 bases at least Q30
Consensus quality: 211541 bases at least Q20

```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1
1598: contig of 1598 bp in length
1599: gap of unknown length
3852: contig of 2154 bp in length
3853: gap of unknown length
3952: gap of unknown length
5420: contig of 1468 bp in length
3953: gap of unknown length
5520: gap of unknown length
5521: contig of 6082 bp in length
11603: contig of 11702 bp in length
11603: gap of unknown length
11703: contig of 7270 bp in length
18972: contig of 19072 bp in length
19073: gap of unknown length
25594: contig of 6522 bp in length
25595: gap of unknown length
25694: gap of unknown length
34376: contig of 8682 bp in length
34377: gap of unknown length
45748: gap of 11273 bp in length
34477: contig of 45849 bp in length
45849: gap of unknown length
45850: contig of 15140 bp in length
60989: gap of unknown length
61090: contig of 16016 bp in length
77107: gap of unknown length
77108: contig of 16119 bp in length
93326: gap of unknown length
93327: gap of unknown length
93426: gap of unknown length
118266: contig of 24840 bp in length

```

```

* 118267 118366: gap of unknown length
* 118367 145520: contig of 27154 bp in length
* 145521 145620: gap of unknown length
* 145621 178124: contig of 32504 bp in length
* 178125 178224: gap of unknown length
* 178225 215435: contig of 37211 bp in length.
Location/Qualifiers

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FEATURES

source

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1.215435
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-111N17"

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/note="assembly_name:Contig15"
misc_feature 1699.3852
/note="assembly_name:Contig16"
misc_feature 3953.5420
/note="assembly_name:Contig17"
misc_feature 5521.11602
/note="assembly_name:Contig18"
misc_feature 11703.18972
/note="assembly_name:Contig19"
misc_feature 19073.25594
/note="assembly_name:Contig20"
misc_feature 25695.34376
/note="assembly_name:Contig21"
misc_feature 34477.45749
/note="assembly_name:Contig22"
misc_feature 45850.60989
/note="assembly_name:Contig23"
misc_feature 61090.77107
/note="assembly_name:Contig24"
misc_feature 77208.93326
/note="assembly_name:Contig25"
misc_feature 93427.118266
/note="assembly_name:Contig26"
misc_feature 118367.145520
/note="assembly_name:Contig27"
misc_feature 145621.178124
/note="assembly_name:Contig28"
misc_feature 178225.215435
/note="assembly_name:Contig29"
BASE COUNT 58831 a 49369 c 48002 g 57707 t 1526 others
ORIGIN

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Query Match 3.4%; Score 21; DB 2; Length 215435;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 347 CAAAGCTTTTAATTAAAT 367
DB 139645 CAAAGCTTTTAATTAAAT 139665

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RESULT 33
AB073376/c 216734 bp DNA linear VRT 02-MAY-2002
DEFINITION AB073376 BAO00027
ACCESSION AB073376.1 GI:18157518
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryzias latipes (Japanese medaka)
Oryzias latipes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Altheriomorpha;
Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.
1
REFERENCE
Matsuo, M.Y., Asakawa, S., Shimizu, N., Kimura, H. and Nonaka, M.
Nucleotide sequence of the MHC class I genomic region of a teleost,
the medaka (Oryzias latipes)
Immunogenetics 53 (10-11), 930-940 (2002)
JOURNAL

```

```

MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

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21850510
11862394
2 (bases 1 to 216734)
Watsuo, M.Y., Asakawa, S., Shimizu, N., Kimura, H. and Nonaka, M.
Direct Submission
Submitted (19-OCT-2001) Megumi Y Watsuo, University of Tokyo,
Department of Biological Sciences, Graduate School of Science;
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
(E-mail: megabiol.s.u-tokyo.ac.jp, Tel: 81-3-5841-4064,
Fax: 81-3-5841-4064)
Location/Qualifiers

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FEATURES

source

1.216734

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/organism="Oryzias latipes"
/mol_type="genomic DNA"
/strain="Hd-rR"
/db_xref="taxon:8090"

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/clone_id="medaka-fish sperm DNA BAC library"
/note="Linkage Group 11"
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/gene="GNBP"
complement(join(314.459,819.887))
/gene="GNBP"
complement(join(314.459,819.887))
/gene="GNBP"
/note="supported by GENSCAN and homologous to guanine
nucleotide binding protein (gi:121013)"

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CDS

gene

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/evidence-not experimental
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/db_xref="GI:18157519"
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GRVQLKRNKMGHAKIYAMHWSADS"
complement(join(6794.6953,9685.9880,11390.11574,
11734.11895,14226.14313))
/gene="CLEBP"
complement(join(6794.6953,9685.9880,11390.11574,
11734.11895,14226.14313))
/gene="CLEBP"

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gene

CDS

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/note="supported by GENSCAN and partially homologous to
the c-type lectin domain"
/codon_start=1
/evidence-not experimental
/protein_id="BAB83835.1"
/db_xref="GI:18157520"

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/translation="MNSNVAFSKLVDEGNRTLRHRAVDHSDKNSQDDEGTTLM
QTVSALFALISKLQENKQOEKRALALDLITKAPVVSIMSPGVPECP
TWMFLFNSSCYFISTOKMKWRDSQYICORGAHAIHTAEQFTMLPRAHNAAY
WFGISDRKDEEMKWDGTSVEKSFWEGERNNHINDECGIIVTQVLVERVAISWD
APCEMSIYFICEKEMKTQ"
17152.17844
/note="LTR of LReo_3"
17886.22382
/gene="LReo_3"
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/gene="LReo_3"

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LTR

gene

CDS

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/note="LTR retrotransposable element
partially supported by GENSCAN"
/evidence-not experimental
/protein_id="BAB83836.1"
/db_xref="GI:18157521"

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/translation="WTRGKRTETPDLPIDDKATSSHOEGAAAPDEPKLELTLLVVK
TLVQSGARDLVKESARODQRMKNLQHCQOMQOTQYKELKDEFTAEDEDDDD
VGEAGADVQALMTSCGPPTGPILOKQKPLPSPEDDIEHMLTFFERLAVCR
WPKEMWAIQLPILTKARSAVYVMDPDSDEYKVEVILAKYITRATYKRRAL
DINREPTREIRYVRLBELPMKVMVPEACTVEIESEKILLBQFLPMRMEWIERD
PQSAEASRLAEVLSARSGRPVFGDSYFSGRSKSYAERGGQTSRHNANSRPF
SAKAEKSSSSSSQNVRCYQCEIHTQYTCPTKRONPSLCTVPSOPVQVK
EAVTVFVINSQKREKALDSCGFSVVSLSVPRDLNWEATATIGCVGDEKAYRTAE
VYLITGQTVLMPVILVPELPSVILGSDVPLPDLIOAHAKMDGVCERSVQARK
PVGSDHGAIVSCNVTTRANARALBELFPHNTELEISPVKAVKSAORERKFLA
TVRQCDDEKPSHYLDROVADIALAORADPRLKVPMDKVSIEISGQTKRVECLTDK
ITLNGILYQHGVEALAPQCSKRYMGIHGISIPMAGHLAROKSINRIANREVMV
AMVTLKREFCASCEICQLTAPQGVARAPLPPLIETFPDRIIGMDIVGPLEKSSGKH

```

YIIVICDVAITRYPEAFIRSVKAOIANCLIQIFSRNGIPIKEIILTDCGTFNLKLO
VSLGVGKIGITTPYHPQTDGLVERFNQTLTKMLRKFSVEGADMDQLPYLIPAYRE
VPOASTGSPPELLYGRQVRLDLKDYMEKPYTDKNVSVYLKMEERLSTILA
OEHMSAOAOOKTWYDKKARDRIPOVGQOVLLPTSDNKLAMQGVYSITKLGEV
TYELIYMEPKLKHQRHYNLKEROLFPSNMKOECONTLFTVADDEBERKLPHEE
MASSPVYSHLOPKOREVGRLLDLEFKETPGFTLLVQKHVHLKEDVPRRRYRIP
ERLVVKEKEIEMLKLGIVIEPSTSEWCSPVALVPKQDGLRFCIDEPYLVNAVKIOS
YPMRIBELBELVEGSKETITLIDYKQVLAQETKELTAFTTPYKGFQPKMPFG
LOGAPATFORLMEIDILRDFPOFAAYLDDVLIIFSHSDHMSHLRHLIKAGLTI
NKGCVAAQOOVEYLHVGQVGVKPYRGVIOEYOIPTTKKKVRAFGVLQWYMSK
FIRHPADRAALVTLDTLRASAPNKVYWTEDCAAFDKGALTSSSVLYSPFTFPIIL
OTDSAVGLGAVLVOEABGERHPVLFSLKLDRETRYSTVEKCLAKMKADLRLRY
LLGRFCLETHRALQWLRMKDSNTRLTAYLISQAVDFTVQYRAKTCNVADCLSR
VHEN"

LTR
/note="LTR of LReO 3"
complement (join(23657..23844,24033..24365,24473..24751,
26771..27052,27490..27568))
/gene="Otlaci-S4"
comp (join(23657..23844,24033..24365,24473..24751,
26771..27052,27490..27568))
/gene="Otlaci-S4"
/note="non-classical class Ib
partially supported by GENSCAN and Grailexp"
/codon_start=1
/evidence=not experimental
/protein_id="BAB83837.1"
/db_xref="GI:18157523"
/translation="MKCKMLKCDPLANTYIOKSKQFYMTRKHSLEVECTAAGVKEP
PEFVGATVDKDFVSGSMILHRTPEKSTVTKFIDENSKOIMWYTTCKEKEPVAS
I1IDGKHLNQNTWYKSVKHFQOHSCEWDEDEGTFENRRAVYDEDLKIDLK
HEWALTLEKAYATKLTWENKSVLSKHSSEYFSIQCPDWLKCYVTFGRYDLOAVLPLV
SLORNSLSLSCHATGFPFDIADLFMMKDGEEFHDVEKESILPNNDETOMSYLN
TSSLPLDMOKSECVFOLFSSOKNITVSLDKTKIRTDNATGVMCSGNDSTFKHWMGA
GTALFIYVMAVSSNMFKRLNLNOCYCSCSDKKNKDVNGSICPOVYSEEN"
join(52614..52763,53361..53514,53616..53795,57879..58039,
58223..58346,60583..60715,66607..66642,68636..68727,
68889..68994,69164..69311)
/gene="RXRB"
join(52614..52763,53361..53514,53616..53795,57879..58039,
58223..58346,60583..60715,66607..66642,68636..68727,
68889..68994,69164..69311)
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/db_xref="GI:18157523"
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PISPOINSTVMSGLHTVSSSDVYKPLGLKOLSHSGPMLSGKRCSICGPRSSG
KHGYVSGCGGKPFRTVRKDLTYTCGNDNDCTYGRQORRCOROKOLANGMKR
EAVQERORNKREBEVSTAVNEEMVEKILBNMAVEOKTELHSGSGSSGSPND
FVNISQADKQLFTLVEMAKRIPHSFLPDDOVLILNMBELIASHSISKSPD
LILATGLHVRNNSAHSAAGVAFIDRAHNAEAGALFERVLTYSKMRQMDKELGSC
LRLAILENPDADKLSNSEVELLRERYAVETAYKHYCPQGGFALCLRLRLARS
IGLCKLEHLFFFKLIGTPIPTFLMEMLEAPHLR"

gene
join(100457..100538,103270..103431,104635..104845,
105409..105571,105691..105813,109660..110049,
110248..110403,110560..110637,115214..115267,
116168..116209,116401..116463,116661..116735,
116910..116996,117362..117418,117612..117665,
117858..117911,118128..118181,118484..118537,
118670..118723,118800..118844,119050..119103,
121738..121782,121933..121986,122392..122436,
124339..124392,124502..124546,124763..124816,
124954..124998,125091..125144,125308..125315,
127044..127097,127222..127275,127428..127472,
127866..127919,128078..128122,128244..128297,
128741..128794,129460..129513,129679..129676,
130300..130353,130559..130666,130761..130872,
131008..131048,131203..131256,131363..131470,
131591..131644,131728..131781,132041..132094,

CDS

132175..132228,132324..132431,132521..132574,
132692..132745,132830..132883,133086..133139,
133571..133678,133778..133831,133966..134157,
134251..134304,134385..134420,134521..134574,
134667..134952,135086..135195,136338..136574,
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105409..105571,105691..105813,109660..110049,
110248..110403,110560..110637,115214..115267,
116168..116209,116401..116463,116661..116735,
116910..116996,117362..117418,117612..117665,
117858..117911,118128..118181,118484..118537,
118670..118723,118800..118844,119050..119103,
121738..121782,121933..121986,122392..122436,
124339..124392,124502..124546,124763..124816,
124954..124998,125091..125144,125308..125315,
127044..127097,127222..127275,127428..127472,
127866..127919,128078..128122,128244..128297,
128741..128794,129460..129513,129679..129676,
130300..130353,130559..130666,130761..130872,
131008..131048,131203..131256,131363..131470,
131591..131644,131728..131781,132041..132094,
132175..132228,132324..132431,132521..132574,
132692..132745,132830..132883,133086..133139,
133571..133678,133778..133831,133966..134157,
134251..134304,134385..134420,134521..134574,
134667..134952,135086..135195,136338..136574,
137391..137528)
/gene="COL11A2"
/note="collagen type XI alpha 2
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/codon_start=1
/evidence=not experimental
/protein_id="BAB83839.1"
/db_xref="GI:18157524"
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CDS

gene

Query Match 3.4%; Score 21; DB 5; Length 216734;
Best Local Similarity 100.0%; Pred: No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 14691 ATGCTTATTATTATTTGTTG 14671

RESULT 34
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LOCUS Homo sapiens chromosome X clone RP11-607K23, WORKING DRAFT
DEFINITION
SEQUENCE 19 unordered pieces.
AC021166
AC021166.5 GI:9838294
VERSION HTG: HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 218708)
Waterson,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
2 (bases 1 to 218708)
Waterson,R.H.
REFERENCE Direct Submission
Submitted (14-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108 USA
On Aug 17, 2000 this sequence version replaced gi:8570350.
----- Genome Center -----


```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0607K23
----- Summary Statistics -----
Sequencing vector: M13, 84t
Sequencing vector: plasmid, 16t
Chemistry: Dye-primer ET, 84t of reads
Chemistry: Dye-terminator Big Dye, 16t of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 205213 bases at least Q40
Consensus quality: 209108 bases at least Q30
Consensus quality: 21651 bases at least Q20
Insert size: 219000; agarose-efp
Insert size: 218241; sum-of-contigs
Quality coverage: 4.39 in Q20 bases; agarose-efp
Quality coverage: 4.46 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 2204: contig of 2204 bp in length
* 2305 2304: gap of unknown length
* 2305 4235: contig of 1931 bp in length
* 4236 4335: gap of unknown length
* 4336 7018: contig of 2683 bp in length
* 7019 7118: gap of unknown length
* 7119 10388: contig of 3270 bp in length
* 10389 10488: gap of unknown length
* 10489 15190: contig of 4702 bp in length
* 15191 15290: gap of unknown length
* 15291 22093: contig of 6803 bp in length
* 22094 22193: gap of unknown length
* 22194 32641: contig of 10448 bp in length
* 32642 32742: gap of unknown length
* 32742 40447: contig of 7706 bp in length
* 40448 40547: gap of unknown length
* 40548 52107: contig of 11560 bp in length
* 52108 52207: gap of unknown length
* 52208 61381: contig of 9174 bp in length
* 61382 61481: gap of unknown length
* 61482 74236: contig of 12755 bp in length
* 74237 74337: gap of unknown length
* 74337 86944: contig of 12608 bp in length
* 86945 87044: gap of unknown length
* 87045 100053: contig of 13009 bp in length
* 100054 100153: gap of unknown length
* 100154 112917: contig of 12764 bp in length
* 112918 113017: gap of unknown length
* 113018 126631: contig of 13614 bp in length
* 126632 126731: gap of unknown length
* 126732 141967: contig of 15236 bp in length
* 141968 142067: gap of unknown length
* 142068 160148: contig of 18081 bp in length
* 160149 160248: gap of unknown length
* 160249 179584: contig of 19236 bp in length
* 179585 218708: gap of unknown length
* 218708 39124: contig of 39124 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-607K23"
1. 2204
/note="assembly_name:Contig7"

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Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
Sison,C., Stancirpop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,
Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 226584)
Green,E.D.
Direct Submission
Submitted (04-JUN-2003) NIH Intramural Sequencing Center, 8717
Groveomment Circle, Gaithersburg, MD 20877, USA
Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
Project Information
Center project name: evv
Center clone name: 023K01
Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 223681 bases at least Q40
Consensus quality: 224442 bases at least Q30
Consensus quality: 224838 bases at least Q20
Insert size: 196000; agarose-fp
Insert size: 226084; sum-of-ctctigs
Quality coverage: 14.57x in Q20 bases; agarose-fp
Quality coverage: 12.63x in Q20 bases; sum-of-ctctigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 7401: contig of 7401 bp in length
* 7402 7501: gap of unknown length
* 20595: contig of 13094 bp in length
* 20596 51665: gap of unknown length
* 51666 51765: gap of unknown length
* 51766 97810: contig of 46045 bp in length
* 97811 97910: gap of unknown length
* 97911 127704: contig of 29794 bp in length
* 127705 127804: gap of unknown length
* 127805 226584: contig of 98780 bp in length.
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ORIGIN

Query Match 3.4%; Score 21; DB 2; Length 226584;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 229 TATGCTTATTTATTTATGTT 249
DB 200054 TATGCTTATTTATTTATGTT 200034

RESULT 36
PFA929358
LOCUS
DEFINITION Plasmodium falciparum strain 3D7, chromosome 9; segment 4/5.
ACCESSION AL929358 AL844508
VERSION AL929358.1 GI:23505147
KEYWORDS
SOURCE
ORGANISM Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 254050)
HALL,N., PAIR,A., BERTMAN,M., CHURCHER,C., HARRIS,B., HARRIS,D.,
MUNGALL,K., BOWMAN,S., ALKIN,R., BAKER,S., BARRON,A., BROOKS,K.,
BUCKEE,C.O., BURROWS,C., CHEREVACH,I., CHILLINGWORTH,C.,
CHILLINGWORTH,T., CHRISTODOULOU,Z., CLARK,L., CLARK,R., CORTON,C.,
CROBIN,A., DAVIES,R., DAVIS,P., DEAR,P., DEARDEN,F., DOGGETT,J.,
FELTWEILL,T., GOBLE,A., GOODHEAD,I., GWILLIAM,R., HAMLIN,N.,
HANCE,Z., HARPER,D., HAUSER,H., HORNBY,T., HOLROYD,S.,
HORROCKS,P., HUMPHREY,S., JAGEL,S.K., JAMES,K.D., JOHNSON,D.,
KERTHONOU,A., KNIGHTS,A., KONFOROV,B., KYES,S., LAKE,N.,
LAWSON,D., LEMNARD,N., LINE,A., MADDISON,M., MCLEAN,D., MOONEY,P.,
MOULE,S., MURPHY,L., OLIVER,K., ORMOND,D., PRICE,C., QUAIL,M.A.,
RABINOWITSCH,E., RAJANDREAM,M.A., RUTTER,S., RUTHERFORD,K.M.,
SANDERS,M., SIMMONDS,M., SEEGER,K., SHARP,S., SMITH,R., SQUARES,R.,
SQUARES,S., STEVENS,K., TAYLOR,K., TIVEY,A., UNWIN,L.,
WHITEHEAD,S., WOODWARD,J., SULSTON,J.E., CRAIG,A., NEWBOLD,C. and
Barrell,B.G.
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)
22255708
MEDLINE
12368867
PUBMED
2 (bases 1 to 254050)
SANDERS,M., HAUSER,H., BAKER,S., UNWIN,L., MUNGALL,K., BERTMAN,M.,
PAIR,A., HALL,N., BOWMAN,S., CHURCHER,C., QUAIL,M. and Barrell,B.
Direct Submission
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
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763..2532
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3a, subunit 3, 60kd TR:AAH09141 (EMBL:BC009141) (501 aa)
fasta scores: E(): 1.7e-24, 30.75e4 id in 595 aa. No
significant pfam hit; SMART hit to SM00355, zinc
finger;Profilscan hit to PSS0171, Zn-finger (C2H2) in
matrix and other RNA-binding proteins"
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YIPRYCKTRNESEYKSYVENLNTYMSFPEKIVLVDCKTTYKEVEDDPYNNKKEIK
GWEKYTYDLPFCINNNKLYASBGTQSYLKKCKYNDNDKTYLANKRYVEQLEIKRN
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EOKLGGTLISNNININENYTIYNTKKEHIIYIYVYVYFICLCSFYFYMYILS
COVLNTHRWLNRIYKSNKLYMCVRLKIKMKGSIQRHFCFLFMPNHFIYFNNYKNY
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(Signal peptide probability 0.001, signal anchor
probability 0.995) with cleavage site probability 0.001
between residues 27 and 28
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IHDTHNEAYKYVADLENNKKYKCKKKKIENSPEIYNSLFRYINENYATNSSEYVON
KLNQTKVNNIYHQGYKQKKNKPNHPSITIIKHKKYFNKKNKADJGCBGAEART
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35.21% id in 213 aa, and to Escherichia coli prolyl-L-erna
synthetase pros or drpa or b0194 SMALL:SYP_ECOLI
(SMALL:p16659) (572 aa) fasta scores: E(): 7.3e-08, 31.91%
id in 235 aa. Pfam match to PF00587, tRNA synthetase class
II (G, H, P, S and T)
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(Signal peptide probability 0.720, signal anchor
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RESULT 37
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DEFINITION Drosophila melanogaster chromosome 2R, section 23 of 74 of the

complete sequence.

ACCESSION AE003827 AE002787 AE013599

VERSION AE003827.3 GI:21627498

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 256227)

Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D.,
Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabot,G.L.,
Abrill,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Balabin,D.,
Ballew,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M.,
Beeson,K.Y., Bens,P.V., Berman,B.P., Bhandari,D., Bolshakov,S.,
Borkova,D., Botchan,M.R., Bock,J., Brokstein,P., Brotter,R.,
Burris,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A.,
Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B.,
Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mayhew,A.D., Dew,I.,
Diez,S.M., Dodson,K., Doup,L.E., Downe,M., Dugan-Rocha,S.,
Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferrara,S.,
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Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J.,
Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J.,
Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z.,
Kernson,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Matesi,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Murny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Nusken,D.R., Paclebo,J.M., Palazolo,M., Peltman,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Stimpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Svitzkas,R., Tector,C., Turner,R.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodruff,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.

The genome sequence of *Drosophila melanogaster*

Science 287 (5461), 2185-2195 (2000)

20196006

JOURNAL

MEDLINE

PUBMED

REFERENCES

AUTHORS

2 (bases 1 to 256227)
Celniker,S.E., Adams,M.D., Krommiller,B., Wan,K.H., Holt,R.A.,
Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y.,
Bannon,J., An,H., Baldwin,D., Bannion,J., Beeson,K.Y., Busam,D.A.,
Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farrant,D.,
Fertiera,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A.,
Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J.,
Phouaneavong,S., Pletman,G.S., Puri,V., Richards,S., Scheeler,F.,
Stapleton,M., Strong,R., Svitzkas,R., Tector,C., Tyler,D.,
Williams,S.M., Zaveri,J.S., Smith,H.O., Venter,J.C. and Rubin,G.M.

TITLE
JOURNAL
REFERENCE
AUTHORS
3 (bases 1 to 256227)

Sequencing of *Drosophila melanogaster* genome
Unpublished
Matera,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L.,
Campbell,K., Hradecky,P., Huang,Y., Kaminker,J.S., Prochnik,S.E.,
Smith,C.D., Tupy,J.L., Bergman,C.M., Berman,B.P., Carlson,D.W.,
Celniker,S.E., Clamp,M.E., Drysdale,R.A., Emmert,D., Frise,E., de
Grey,A.D.N.J., Harris,N.L., Krommiller,B., Marshall,B.,
Millburn,G.H., Richter,J., Russo,S., Seale,S.M.J., Smith,E.,
Shu,S., Smutnick,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M.,
Rubin,G.M., Mungall,C.J. and Lewis,S.E.

TITLE

JOURNAL

REFERENCE

AUTHORS

CONSRPTM

TITLE

JOURNAL

REFERENCE

AUTHORS

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REFERENCE

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TITLE

JOURNAL

REFERENCE

AUTHORS

1. 256227
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 38
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HUCUS004605

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DEFINITION Homo sapiens Chromosome 16 BAC clone CIT9878K-A-248F7, complete
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ORGANISM Homo sapiens
REFERENCE
    1 (bases 1 to 259474)
    Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
    Fuhrman,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
    Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.D., Mitchell,S.,
    Eichler,B.B., Harris,P.C., Venter,J.C. and Adams,M.D.
    Genome duplications and other features in 12 Mb of DNA sequence
    from human chromosome 16p and 16q
    Genomics 60 (3), 295-308 (1999)
JOURNAL
    MEDLINE 99425270
    PUBMED 10493829
AUTHORS
    2 (bases 1 to 259474)
    Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J.,
    Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.
    Homo sapiens Chromosome 16 BAC clone CIT9878K-A-248F7
    Unpublished
    3 (bases 1 to 259474)
    Adams,M.D. and Loftus,B.J.
    Direct Submission
    Submitted (23-APR-1998) The Institute for Genomic Research, 9712
    Medical Center Dr, Rockville, MD 20850, USA, Email:
    bjoftus@igrr.org
    4 (bases 1 to 259474)
    Adams,M.D. and Loftus,B.J.
    Direct Submission
    Submitted (24-JUL-1998) The Institute for Genomic Research, 9712
    Medical Center Dr., Rockville, MD 20850, USA
    On Jul 24, 1998 this sequence version replaced gi:3228501.
    Address all correspondence to: Mark Adams The Institute for Genomic
    Research 9712 Medical Center Dr, Rockville, MD 20850, USA e-mail
    address: humen@igrr.org. The orientation of the sequence is from
    SP6 end to 3' end. Genes were identified by a combination of five
    methods including: XGRAL (available by anonymous ftp from
    athur.epm.ornl.gov), GeneFinder (Phil Green, University of
    Washington), Genscan (Chris Burge,
    http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the
    complete sequence against a peptide database and the Human gene
    index database at TRIGR (http://www.igrr.org/tbgi/ngi.html).
    Genes without peptide homology having spliced EST hits are termed
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RESULT 40	
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LOCUS	DROWTM2 172 bp DNA linear INV 24-MAR-2000
DEFINITION	Drosophila melanogaster ribosomal RNA large subunit ribosomal RNA (mt:rRNA) gene, partial sequence; and unknown gene; mitochondrial genes for mitochondrial products.
ACCESSION	J01409.1 GI:336812
VERSION	2 of 2
KEYWORDS	mitochondrion Drosophila melanogaster (fruit fly)
SOURCE	Drosophila melanogaster
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyrididae; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 172) Clary,D.O., Goddard,J.M., Martin,S.C., Fauron,C.M. and Wolstenholme,D.R. Drosophila mitochondrial DNA: a novel gene order Nucleic Acids Res. 10 (21), 6619-6637 (1982)
TITLE	83090428 6294611 2 (bases 1 to 172) de Bruijn,M.H. Drosophila melanogaster mitochondrial DNA, a novel organization and genetic code Nature 304 (5923), 234-241 (1983)
MEDLINE	83245048 6408489
PUBMED	
COMMENT	Compared with mouse, human, and bovine mitochondrial genomes. The order of genes is different in Drosophila and mammalian mitochondria. Corresponding genes also appear on different strands. The codon 'aga' codes for arginine in Drosophila and is not present or is a termination codon in the mammals. 'tga' codes for tryptophan rather than termination. Origin of replication is located within the 'at' rich region approx 250-450 bp from the 5' boundary. The 'at' rich region varies in size between strains and species of Drosophila and does not appear to be transcribed. The direction of replication is in the same direction as transcription of all genes in this segment.
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567	AATAGTACTGTGTTTAAATA 586

Wed Oct 8 12:17:09 2003

us-10-010-160-1.oligo.rge

Page 45

Db 165 AATAGTACTGTTTATATA 146

Search completed: October 8, 2003, 07:18:40
Job time : 2081 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 03:11:35 ; Search time 218 Seconds
(without alignments)
7702.066 Million cell updates/sec

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Title: US-10-010-160-1
Perfect score: 622
Sequence: 1 atgctgatgaccagaa.....aattattcgatcgagatc 622
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scoring table: OLIgo_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

word size :

Total number of hits satisfying chosen parameters: 5105512

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 1000 summaries

Database : N_Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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C	3	19	3.1	390	22	ABM58347		Human foetal liver
C	4	19	3.1	390	22	ABK27469		Probe #5935 for ge
C	5	19	3.1	390	22	ABK06446		Human brain expres
C	6	19	3.1	390	22	AAK32124		Human bone marrow
C	7	19	3.1	390	22	AAI15859		Probe #5892 for ge
C	8	19	3.1	390	22	AAI37975		Probe #6661 used t

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C	10	19	3.1	390	24	AB506891
C	11	19	3.1	633	24	ABN677186
C	12	19	3.1	948	25	ACA948580
C	13	19	3.1	989	21	AAA988731
C	14	19	3.1	989	21	AAA98155
C	15	19	3.1	989	24	AAA298848
C	16	19	3.1	1061	22	AA126601
C	17	19	3.1	1908	8	AA271064
C	18	19	3.1	2422	22	AA530510
C	19	19	3.1	2422	22	AA530511
C	20	19	3.1	2422	22	AA106289
C	21	19	3.1	2422	22	AA106290
C	22	19	3.1	3318	25	ABX63452
C	23	19	3.1	4357	23	ABL15016
C	24	19	3.1	4464	23	ABL269696
C	25	19	3.1	5694	25	ABX445116
C	26	19	3.1	5849	19	AAV33135
C	27	19	3.1	10468	22	AA930509
C	28	19	3.1	10468	22	AA930512
C	29	19	3.1	10468	22	AA106288
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C	31	19	3.1	37515	24	ABO666957
C	32	19	3.1	51959	24	ABO969677
C	33	19	3.1	349980	22	AAH68529
C	34	19	3.1	349980	22	AAH68530
C	35	19	3.1	513445	22	AA161373
C	36	19	3.1	1503841	24	ABT00100
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C	38	19	3.1	1503800	22	AAK95524
C	39	19	3.1	1503800	22	AAK96737
C	40	19	3.1	1691080	24	ABX08333
C	41	18	2.9	47	21	AAZ67966
C	42	18	2.9	69	14	AAQ41022
C	43	18	2.9	73	14	AAQ41033
C	44	18	2.9	73	14	AAQ41038
C	45	18	2.9	87	14	AAQ41022
C	46	18	2.9	90	14	AAQ41023
C	47	18	2.9	104	7	AAAN60057
C	48	18	2.9	104	15	AAO67968
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C	52	18	2.9	357	22	ABAI18083
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C	56	18	2.9	561	22	ABX377888
C	57	18	2.9	1440	22	AA531218
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C	76	18	2.9	4515	23	ABV26511
C	77	18	2.9	4515	23	ABV282248
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C	88	2.9	6710	21	AAZ59981	Intermediate plaam
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C	92	2.9	8333	24	ABL33502	Human immune syste
C	93	2.9	8333	24	ABK28255	DNA transcription
C	94	2.9	8710	16	AAQ89650	PSCI1 FIPV E1. Sy
C	95	2.9	9020	16	AAQ7652	PSCI1 FIPV N. Syn
C	96	2.9	16200	24	AAQ6438	Mouse l66 genomic
C	97	2.9	17538	24	ABL33157	Human immune syste
C	98	2.9	19459	24	ABL70527	Chemically treated
C	99	2.9	19459	24	ABK31212	Signal transductio
C	100	2.9	22341	23	ABL03352	Drosophila melanog
C	101	2.9	28310	23	ABL16222	Drosophila melanog
C	102	2.9	32150	22	AA532454	Human genomic DNA
C	103	2.9	33632	23	ABL29040	Drosophila melanog
C	104	2.9	50000	20	AAK33517	Human kidney amino
C	105	2.9	51352	24	AA56607	Human kidney amino
C	106	2.9	62909	22	AAK28545	Genomic fragment #
C	107	2.9	640681	24	ABA92787	Buchnera sp. genom
C	108	2.7	205	21	AAI2545	Human secreted pro
C	109	2.7	218	21	AAI0055	Human secreted pro
C	110	2.7	226	21	AAK01546	Human death domain
C	111	2.7	228	19	AAV61471	DR5-related clone
C	112	2.7	304	22	AAK6338	Human immune/haema
C	113	2.7	328	21	AAK17938	Human secreted pro
C	114	2.7	351	22	AAK6338	Human secreted pro
C	115	2.7	401	22	AAI88370	Human polynucleoti
C	116	2.7	438	22	AA534352	Human polynucleoti
C	117	2.7	467	22	ABK07414	Human cDNA encodin
C	118	2.7	467	22	AAK91145	Human pancreatic c
C	119	2.7	469	22	AAK91145	Human pancreatic c
C	120	2.7	469	22	AAK88801	Human pancreatic c
C	121	2.7	481	22	AAH68767	Human digestive sy
C	122	2.7	486	24	ABN64591	Human digestive sy
C	123	2.7	503	24	ABQ49868	Human cancer relat
C	124	2.7	503	24	ABQ49868	Oligonucleotide fo
C	125	2.7	526	25	ABZ36766	Oligonucleotide fo
C	126	2.7	528	22	AAH72479	Human GENSER codin
C	127	2.7	528	24	ABV87835	Human cervical can
C	128	2.7	533	24	ABQ19690	Human colon cancer
C	129	2.7	533	24	ABQ19691	Oligonucleotide fo
C	130	2.7	560	22	AAI90189	Oligonucleotide fo
C	131	2.7	567	20	AAK20735	Human polynucleoti
C	132	2.7	591	22	AAH70195	Polynucleotide seq
C	133	2.7	593	23	AAV57571	Human cervical can
C	134	2.7	605	22	AAK72050	Human prostate exp
C	135	2.7	618	22	AAH11934	Human immune/haema
C	136	2.7	618	24	ABQ30468	Human cDNA clone (
C	137	2.7	618	24	ABQ30469	Oligonucleotide fo
C	138	2.7	683	24	ABN99400	Oligonucleotide fo
C	139	2.7	683	24	AAI48821	Human secreted pro
C	140	2.7	694	21	AAAO1638	Murine anergy mark
C	141	2.7	735	24	ABQ33542	Human colon cancer
C	142	2.7	735	24	ABQ33543	Oligonucleotide fo
C	143	2.7	750	24	ABZ32208	Oligonucleotide fo
C	144	2.7	750	24	ABZ32208	Oligonucleotide fo
C	145	2.7	773	22	ABQ6593	Candida albicans e
C	146	2.7	776	22	AAH05122	C. albicans BAX-as
C	147	2.7	776	22	AAH05122	Human ovarian anti
C	148	2.7	802	22	AAI23739	Drosophila melanog
C	149	2.7	908	22	AAH29752	Human breast cance
C	150	2.7	914	24	ABQ25670	Aspergillus oryzae
C	151	2.7	914	24	ABQ25671	S. cerevisiae apopt
C	152	2.7	1248	24	ABZ12493	Oligonucleotide fo
C	153	2.7	1265	24	ABQ76369	Oligonucleotide fo
C	154	2.7	1337	25	ACA56384	S. cerevisiae BAX-Mouse signalling p

228	17	2.7	5851	24	ABN83957	Human gene sequenc	c 301	16	2.6	201	24	ABN93304	Staphylococcus epi
229	17	2.7	5929	24	ABL32709	Human immune syste	302	16	2.6	204	20	AAV89255	EST clone BP284.
230	17	2.7	6069	24	ABL70440	Chemically treated	303	16	2.6	235	21	AAA1853	Human secreted exp
231	17	2.7	6069	24	AAS61381	Human gene regulat	c 304	16	2.6	241	21	AAK1865	Human secreted pro
232	17	2.7	6069	24	ABK31467	Signal transductio	c 305	16	2.6	251	19	AAK1861	Human biallelic po
233	17	2.7	6096	24	ABK92513	Human prostate spe	c 306	16	2.6	251	19	AAK1862	Human biallelic po
C 234	17	2.7	6113	24	ABL32802	Human immune syste	307	16	2.6	258	25	ABX25181	Human GDP-mannose
C 235	17	2.7	6226	23	ABL27730	Drosophila melanog	308	16	2.6	269	22	AA527946	Novel cDNA encodin
C 236	17	2.7	6227	24	ABL70176	Chemically treated	309	16	2.6	274	23	AA586314	DNA encoding novel
C 237	17	2.7	6227	24	ABL34499	Human metastasis a	310	16	2.6	286	25	ABX26227	Human GDP-mannose
C 238	17	2.7	6531	24	ABL32640	Human immune syste	311	16	2.6	292	24	ABL83926	Human ovarian canc
C 239	17	2.7	6846	19	AAV52331	Streptococcus pneu	c 312	16	2.6	299	23	ABV61855	Human prostate exp
C 240	17	2.7	6853	24	ABL54332	Chemically treated	c 313	16	2.6	307	22	AA537953	Human cDNA encodin
C 241	17	2.7	6915	23	ABL32311	Human immune syste	c 314	16	2.6	314	24	AAAD28996	Buglia neritina KS
C 242	17	2.7	6915	23	ABL07524	Drosophila melanog	c 315	16	2.6	315	24	AAAD28998	Buglia neritina KS
C 243	17	2.7	6929	24	ABL34158	Human immune syste	c 316	16	2.6	318	22	AA180375	Human polynucleoti
C 244	17	2.7	7321	24	ABL70386	Chemically treated	c 317	16	2.6	321	13	AAQ26718	Encodes exon VI of
C 245	17	2.7	7321	24	AAS61338	Human gene regulat	c 318	16	2.6	330	16	AAAT25130	Human gene signatu
C 246	17	2.7	7321	24	ABK31425	Signal transductio	c 319	16	2.6	337	22	AA512430	DNA encoding 1-amt
C 247	17	2.7	7573	18	AA158681	DNA encoding human	c 320	16	2.6	352	24	ABQ97063	Mouse ES cell rela
C 248	17	2.7	7573	18	ABK83875	Human cDNA differe	c 321	16	2.6	375	22	AAK78834	Human immune/haema
C 249	17	2.7	7573	24	ABN95697	Gene #1295 used to	c 322	16	2.6	391	22	AAK75457	Human immune/haema
C 250	17	2.7	7849	24	ABL92279	Chemically treated	323	16	2.6	396	22	ABA70405	Human foetal liver
C 251	17	2.7	7849	24	AAD22330	Chemically treated	324	16	2.6	396	22	ABA57065	Probe #1531 for g
C 252	17	2.7	7900	22	AAS46759	Tumour suppressor	325	16	2.6	396	22	AAK18645	Human brain expres
C 253	17	2.7	9032	22	ABL18256	Drosophila melanog	326	16	2.6	396	22	AAK44573	Human bone marrow
C 254	17	2.7	9110	24	ABL34429	Human immune syste	327	16	2.6	396	22	AA124923	Probe #14856 for g
C 255	17	2.7	9667	23	ABL19960	Drosophila melanog	328	16	2.6	396	22	AA150556	Probe #19242 used
C 256	17	2.7	10183	22	AAS46752	Tumour suppressor	329	16	2.6	396	22	AB544231	Human liver bingle
C 257	17	2.7	11046	24	ABK31537	Signal transductio	330	16	2.6	396	24	AB518810	Human genome-deriv
C 258	17	2.7	13784	24	ABK40061	Human chemically p	c 331	16	2.6	398	22	AA192252	Human polynucleoti
C 259	17	2.7	14847	23	ABL02458	Drosophila melanog	c 332	16	2.6	402	23	ABV13541	Human prostate exp
C 260	17	2.7	15817	23	ABL08312	Drosophila melanog	c 333	16	2.6	410	25	AA187346	Bovine EST associa
C 261	17	2.7	17211	24	ABL32654	Human immune syste	c 334	16	2.6	419	22	AA187346	Human polynucleoti
C 262	17	2.7	21747	23	ABL09060	Drosophila melanog	c 335	16	2.6	420	23	ABV15141	Human prostate exp
C 263	17	2.7	23109	22	AAK82298	Human immune/haema	336	16	2.6	423	22	AAK78273	Human immune/haema
C 264	17	2.7	24259	22	AAS46691	Tumour suppressor	337	16	2.6	424	20	AAK21122	Human immune/haema
C 265	17	2.7	24401	23	ABL03396	Drosophila melanog	c 338	16	2.6	430	25	ABX54123	Polynucleotide seq
C 266	17	2.7	28470	22	AAK71445	Human immune/haema	c 339	16	2.6	435	22	ABX54955	Bovine EST associa
C 267	17	2.7	28482	25	ABZ73855	Secreted protein g	c 340	16	2.6	441	25	ABX54060	Bovine EST associa
C 268	17	2.7	32681	25	ABZ73854	Secreted protein g	c 341	16	2.6	445	21	ABAI6413	Human nervous syst
C 269	17	2.7	32681	25	ABZ74517	Secreted protein g	c 342	16	2.6	451	21	AAK37054	Arabidopsis thalia
C 270	17	2.7	32681	25	ABZ68053	Human secreted pro	c 343	16	2.6	457	21	AAK66002	Human lung cancer-
C 271	17	2.7	47108	24	ABK31510	Signal transductio	c 344	16	2.6	457	24	ABO92407	Human lung cancer
C 272	17	2.7	80578	22	AAH44800	Human GPCR protein	c 345	16	2.6	457	24	AB149221	Human polynucleoti
C 273	17	2.7	90220	24	ABK83576	Human cDNA differe	c 346	16	2.6	462	22	ABA20650	Human nervous syst
C 274	17	2.7	90541	24	ABSS52847	Human SR protein-s	c 347	16	2.6	462	22	AA541700	Genomic sequence #
C 275	17	2.7	92638	24	ABO88096	Human osteoblast d	348	16	2.6	470	22	ABA42791	Human foetal liver
C 276	17	2.7	95500	24	AAD41740	Human RECQL2 DNA #	349	16	2.6	470	22	ABA53219	Human foetal liver
C 277	17	2.7	100000	24	ABO74541	Human transglutami	350	16	2.6	470	22	ABA22994	Probe #1460 for ge
C 278	17	2.7	107820	22	AAD16230	Human ATP-binding	351	16	2.6	470	22	AAK01467	Human brain expres
C 279	17	2.7	113033	25	AA154213	SR protein-specific	352	16	2.6	470	22	AAK26915	Human bone marrow
C 280	17	2.7	130480	22	AA125833	R. marinus bacteri	353	16	2.6	470	22	AA111537	Probe #1470 for ge
C 281	17	2.7	147708	24	ABO88154	Human osteoblast d	354	16	2.6	470	22	AA132819	Probe #1505 used t
C 282	17	2.7	150905	25	ABZ80818	Human PAT-2 polymo	355	16	2.6	470	22	AA101455	Probe #1446 used t
C 283	17	2.7	349980	22	AA186431	Pyrococcus abyssi	356	16	2.6	470	23	AB526504	Human liver single
C 284	17	2.7	349980	22	AA186431	C glutamicum codin	357	16	2.6	470	24	AB501513	Human genome-deriv
C 285	17	2.7	659158	25	ABX16390	Mouse high growth	c 358	16	2.6	475	22	AA186356	Human polynucleoti
C 286	17	2.7	1038602	20	AAZ01425	Complete genome se	359	16	2.6	477	23	AA567787	DNA encoding novel
C 287	17	2.7	1691080	24	ABX083036	Human phosphodiester	360	16	2.6	480	21	AAK00685	Human secreted diffe
C 288	17	2.7	1830121	17	AA142063	Haemophilus influe	361	16	2.6	482	24	ABK62674	Rat sequence diffe
C 289	17	2.7	2155561	24	ABN71527	Streptococcus poly	362	16	2.6	488	22	AAK07395	Human bone marrow
C 290	17	2.7	2162598	25	AB556454	Streptococcus pneu	363	16	2.6	488	22	AAK33171	Human bone marrow
C 291	16	2.6	44	22	AAD08544	Vaccinia virus (VV	364	16	2.6	488	22	AA188969	Probe #7655 used t
C 292	16	2.6	50	24	ABZ02185	Human leukocyte ge	365	16	2.6	488	22	AB532916	Human liver single
C 293	16	2.6	50	24	AAD22237	Vaccinia virus p11	366	16	2.6	488	24	AB507996	Human genome-deriv
C 294	16	2.6	51	22	AA178734	Human silent SNP c	367	16	2.6	490	20	AA532438	Human cDNA encodin
C 295	16	2.6	51	22	AA178735	Human silent SNP c	368	16	2.6	493	20	AAK13759	Enterococcus faeca
C 296	16	2.6	65	24	ABN52782	Mouse spliced tran	369	16	2.6	493	25	AB599554	Enterococcus faeca
C 297	16	2.6	111	24	AAD22235	Vaccinia virus p11	370	16	2.6	493	25	AB524272	Aeperyllus oryzae
C 298	16	2.6	140	22	AAK24374	Human brain expres	c 371	16	2.6	496	21	AAK13173	Plant microsatelli
C 299	16	2.6	140	22	AA156365	Probe #25051 used	372	16	2.6	496	22	ABA57789	Human foetal liver
C 300	16	2.6	155	21	AA156365	Human breast and o	373	16	2.6	496	22	ABA27150	Probe #5616 for ge

374	16	2.6	496	22	AAK05858	Human brain expres	C 447	16	2.6	640	22	AAI62984	Human kidney relat
375	16	2.6	496	22	AAK1492	Human bone marrow	C 448	16	2.6	642	22	AAS30770	Human cDNA encodin
376	16	2.6	496	22	AAI15699	Probe #5632 for ge	C 449	16	2.6	642	22	ABZ51977	Aspergillus oryzae
377	16	2.6	496	22	AAI37374	Probe #6060 used t	C 450	16	2.6	656	22	AAI06053	Human reproductive
378	16	2.6	496	23	ABSI1174	Human liver single	C 451	16	2.6	656	23	ABL98618	Human testicular a
379	16	2.6	496	23	ABVI1393	Human prostate exp	C 452	16	2.6	660	24	ABO55999	Human ovarian anti
380	16	2.6	496	24	ABSO6246	Human genome-deriv	C 453	16	2.6	666	22	AAK91553	Human cDNA 5'-end
381	16	2.6	503	23	ABVO2224	Human prostate exp	C 454	16	2.6	666	22	AAK93123	Human cDNA clone r
382	16	2.6	504	24	ABO32850	Oligonucleotide fo	C 455	16	2.6	696	24	ABN92707	Human cDNA clone r
383	16	2.6	504	24	ABO32851	Oligonucleotide fo	C 456	16	2.6	700	22	AAH70572	Staphylococcus epi
384	16	2.6	505	20	AAV99730	Human foetal brain	C 457	16	2.6	704	21	AAAC43752	Human cervical can
385	16	2.6	513	21	AA43861	Human secreted exp	C 458	16	2.6	707	24	ABO41063	Oligonucleotide fo
386	16	2.6	513	23	ABW51773	Human prostate exp	C 459	16	2.6	707	24	ABO41063	Oligonucleotide fo
387	16	2.6	525	23	ABK78696	Bacillus clausii g	C 460	16	2.6	709	22	AAS34039	Oligonucleotide fo
388	16	2.6	527	23	ABV32538	Human prostate exp	C 461	16	2.6	723	22	AAH71575	Human cDNA encodin
389	16	2.6	527	23	ABV41463	Human prostate exp	C 462	16	2.6	736	24	ABD28990	Human cervical can
390	16	2.6	532	24	ABO14879	Oligonucleotide fo	C 463	16	2.6	738	21	AAA02249	Human colon cancer
391	16	2.6	533	23	ABV23852	Human prostate exp	C 464	16	2.6	739	22	AAF26890	Beet necrotic yell
392	16	2.6	533	23	ABV29729	Human prostate exp	C 465	16	2.6	746	22	AAF26891	Beet necrotic yell
393	16	2.6	533	24	ABO33248	Oligonucleotide fo	C 466	16	2.6	746	22	AAS41441	cDNA encoding nove
394	16	2.6	533	24	ABO33249	Oligonucleotide fo	C 467	16	2.6	748	22	AAH06667	Human cDNA clone (
395	16	2.6	535	22	AAI19863	Human breast cance	C 468	16	2.6	754	24	ABQ22136	Oligonucleotide fo
396	16	2.6	537	22	AAH11416	Human prostate exp	C 469	16	2.6	754	24	ABQ22137	Oligonucleotide fo
397	16	2.6	538	23	ABV52021	Human CDNA clone (C 470	16	2.6	793	18	AAV04161	Phytophthora caps
398	16	2.6	538	23	ABV52021	Human prostate exp	C 471	16	2.6	796	21	AACT5469	Human ORFX ORF1024
399	16	2.6	545	22	AAH17171	Human cervical can	C 472	16	2.6	822	22	AAI95351	Human neuroblastom
400	16	2.6	545	22	AAH11494	Human CDNA clone (C 473	16	2.6	846	24	AAH06636	Human cDNA clone (
401	16	2.6	549	24	ABK53587	Human eosinophili-m	C 474	16	2.6	846	24	AAH06636	Human metalloprote
402	16	2.6	551	22	AAI86614	Human polynucleoti	C 475	16	2.6	857	24	ABQ23998	Oligonucleotide fo
403	16	2.6	550	22	AAH06039	Human CDNA clone (C 476	16	2.6	857	24	ABQ23999	Oligonucleotide fo
404	16	2.6	555	23	ABV55407	Human prostate exp	C 477	16	2.6	873	13	AAQ23662	Oligonucleotide fo
405	16	2.6	558	22	ABK63359	Human foetal liver	C 478	16	2.6	873	13	AAQ23662	Truncated hepatocy
406	16	2.6	558	22	ABA30563	Probe #9029 for ge	C 479	16	2.6	874	18	AAI78409	cDNA encoding 34kD
407	16	2.6	568	22	AAK1899	Human brain expres	C 480	16	2.6	874	18	AAI78409	34 kilodalton hepa
408	16	2.6	568	22	AAK37602	Human bone marrow	C 481	16	2.6	913	20	AAK01054	Nucleotide sequenc
409	16	2.6	568	22	AAI18357	Probe #8290 for ge	C 482	16	2.6	917	22	AAI23181	Human breast cance
410	16	2.6	568	22	AAI43472	Probe #12158 used	C 483	16	2.6	917	24	ABO15930	Oligonucleotide fo
411	16	2.6	568	23	ABSI37258	Human liver single	C 484	16	2.6	927	22	AAI98932	Oligonucleotide fo
412	16	2.6	568	24	ABSI1587	Human genome-deriv	C 485	16	2.6	927	22	AAI63282	Human excretory re
413	16	2.6	572	24	ABLP9594	Toxicologically re	C 486	16	2.6	929	24	ABSI6416	Human kidney relat
414	16	2.6	576	22	ABN64175	Human cancer relat	C 487	16	2.6	937	23	ABV22590	DNA encoding soybe
415	16	2.6	578	22	ABK64333	Human foetal liver	C 488	16	2.6	937	23	ABV22590	Human prostate exp
416	16	2.6	578	22	ABK31471	Probe #937 for ge	C 489	16	2.6	962	24	ABSI63418	DNA encoding soybe
417	16	2.6	578	22	AAK12797	Human brain expres	C 490	16	2.6	979	24	ABL89923	Human polynucleoti
418	16	2.6	578	22	AAK38523	Human bone marrow	C 491	16	2.6	980	24	ABSI63417	DNA encoding soybe
419	16	2.6	578	22	AAI19322	Probe #9255 for ge	C 492	16	2.6	997	22	AAI71907	Human dthyaocrota
420	16	2.6	578	22	AAI44502	Probe #13188 used	C 493	16	2.6	1001	21	AAH51555	Human PMO related
421	16	2.6	578	24	ABO60695	Human colon cancer	C 494	16	2.6	1023	24	ABSI63419	DNA encoding soybe
422	16	2.6	583	23	ABV53735	Human prostate exp	C 495	16	2.6	1026	21	AAF21781	Human breast and o
423	16	2.6	583	22	AAK11783	Human brain expres	C 496	16	2.6	1041	22	AAS40812	Human encoding nove
424	16	2.6	583	22	AAI43384	Probe #12070 used	C 497	16	2.6	1073	21	AAC93425	Human secreted pro
425	16	2.6	584	22	AAH10769	Human CDNA clone (C 498	16	2.6	1118	20	AAI26916	Human gene express
426	16	2.6	586	24	ABO53376	Oligonucleotide fo	C 499	16	2.6	1236	23	AAI21382	Amplicon 6, 668int
427	16	2.6	586	24	ABO53377	Oligonucleotide fo	C 500	16	2.6	1243	23	ABL20009	Drosophila melanog
428	16	2.6	586	24	ABK62587	Human foetal liver	C 501	16	2.6	1255	25	ABSI6938	Human musculoskele
429	16	2.6	588	22	ABR29912	Probe #8378 for ge	C 502	16	2.6	1269	20	AAI20328	Human encoding nove
430	16	2.6	598	22	AAK10945	Human bone marrow	C 503	16	2.6	1272	24	AAI6976	Borrelia burgdorfe
431	16	2.6	598	22	AAK36797	Human genome-deriv	C 504	16	2.6	1272	24	AAI6977	Human angiotensin a
432	16	2.6	598	22	AAI17651	Human cervical can	C 505	16	2.6	1278	24	AAI6966	Human angiotensin a
433	16	2.6	598	22	AAI42578	Probe #7584 for ge	C 506	16	2.6	1287	24	AAI6966	Human angiotensin a
434	16	2.6	598	23	ABSI6462	Probe #11264 used	C 507	16	2.6	1318	22	AAK51532	Human polynucleoti
435	16	2.6	598	24	ABSI0802	Human liver single	C 508	16	2.6	1319	24	ABK4662	Human cDNA differe
436	16	2.6	603	22	AAH68909	Human genome-deriv	C 509	16	2.6	1323	22	ABN70976	Streptococcus poly
437	16	2.6	604	22	AAH8055	DNA encoding G pro	C 510	16	2.6	1323	22	AAH08464	Human secreted pro
438	16	2.6	609	22	AAH8055	Peppermint plant o	C 511	16	2.6	1335	22	AAH08464	Human secreted pro
439	16	2.6	613	23	ABV51891	Human prostate exp	C 512	16	2.6	1343	22	AAK67011	Human immune/haema
440	16	2.6	615	24	ABK51970	Corn cDNA clone cc	C 513	16	2.6	1347	24	ABN68758	Streptococcus poly
441	16	2.6	615	25	ABK51970	Corn cDNA clone cc	C 514	16	2.6	1356	24	ABO54719	Human ovarian anti
442	16	2.6	630	24	ABO33998	Oligonucleotide fo	C 515	16	2.6	1367	21	AAI69877	Arabidopsis thalia
443	16	2.6	630	24	ABO33999	Oligonucleotide fo	C 516	16	2.6	1370	22	AAI69877	Human protein 17 c
444	16	2.6	633	24	ABN66363	Streptococcus poly	C 517	16	2.6	1382	23	ABK42366	Genomic sequence #
445	16	2.6	633	24	ABN70300	Streptococcus poly	C 518	16	2.6	1400	22	AAI69877	Human cDNA encodin
446	16	2.6	640	22	AAI98588	Human excretory re	C 519	16	2.6	1416	24	AAS16973	Human recombinant

C 520	16	2.6	1428	24	AA516971	Human recombinant
C 521	16	2.6	1434	21	AA59740	Human secreted pro
C 522	16	2.6	1434	25	AB273345	Secreted protein-e
C 523	16	2.6	1434	25	AB266953	Human secreted pro
C 524	16	2.6	1460	23	AB16339	Drosophila melanog
C 525	16	2.6	1471	22	AA522543	Human cDNA encodin
C 526	16	2.6	1480	22	AAK94095	Human full-length
C 527	16	2.6	1492	22	AAH54313	S. epidermidis gen
C 528	16	2.6	1498	23	AB155389	Human serine oxida
C 529	16	2.6	1518	24	AB231728	Candida albicans e
C 530	16	2.6	1545	24	ABQ67136	Human angiotensin
C 531	16	2.6	1552	21	AAZ50890	Human receptor-ass
C 532	16	2.6	1566	25	ABX63141	Human cDNA #141 d
C 533	16	2.6	1575	23	AA553208	Enterococcus faeca
C 534	16	2.6	1584	24	ABK74549	Bacillus lichenifo
C 535	16	2.6	1590	23	AB120175	Drosophila melanog
C 536	16	2.6	1591	21	AAZ95204	Human UGT2B7 exon
C 537	16	2.6	1605	24	ABQ69120	Listeria monocytog
C 538	16	2.6	1641	20	AAK13519	Enterococcus faeca
C 539	16	2.6	1641	24	AB599314	Enterococcus faeca
C 540	16	2.6	1659	22	AAH72850	Human cervical can
C 541	16	2.6	1660	23	AA584983	DNA encoding novel
C 542	16	2.6	1661	12	AAQ13398	Human hepatocyte g
C 543	16	2.6	1661	13	AAQ22144	Human HGF gene par
C 544	16	2.6	1661	22	AAH44784	Hepatocyte growth
C 545	16	2.6	1677	25	ABX63140	Human cDNA #140 d
C 546	16	2.6	1679	22	AA512436	DNA encoding 1-ami
C 547	16	2.6	1679	22	AA512440	HGF-WSP hybrid pro
C 548	16	2.6	1692	20	AAK87663	Human recombinant
C 549	16	2.6	1695	24	AA516965	Human T cell recep
C 550	16	2.6	1708	22	ABA09166	Borrelia burgdorfe
C 551	16	2.6	1717	20	AAK20311	Hepatocyte growth
C 552	16	2.6	1725	20	AAK87662	Human secreted pro
C 553	16	2.6	1750	22	AA501461	DNA encoding novel
C 554	16	2.6	1772	23	AA586242	Human nervous syst
C 555	16	2.6	1779	22	ABA19142	Genomic sequence #
C 556	16	2.6	1799	22	AA528340	Human nervous syst
C 557	16	2.6	1827	22	ABA19141	Genomic sequence #
C 558	16	2.6	1780	22	AA528339	Genomic sequence #
C 559	16	2.6	1782	23	AA580222	DNA encoding novel
C 560	16	2.6	1798	22	AAH15479	Human cDNA sequenc
C 561	16	2.6	1805	22	AAH17391	Human cDNA sequenc
C 562	16	2.6	1827	24	AB551815	Novel human thromb
C 563	16	2.6	1839	22	AA102708	Human reproductive
C 564	16	2.6	1861	22	AAH17437	Human cDNA sequenc
C 565	16	2.6	1867	23	ABV21406	Human prostate exp
C 566	16	2.6	1867	23	ABV27224	Human prostate exp
C 567	16	2.6	1883	23	AB15593	Drosophila melanog
C 568	16	2.6	1884	24	AB214431	Arabidopsis thalia
C 569	16	2.6	1901	22	AAH15963	Human cDNA sequenc
C 570	16	2.6	1929	22	AB213304	Arabidopsis thalia
C 571	16	2.6	1938	23	AB554948	cDNA encoding huma
C 572	16	2.6	1956	21	AAAZ7325	Impatiens balsamita
C 573	16	2.6	1980	20	AAK58808	Human leukaemia-as
C 574	16	2.6	1983	22	AAH18363	Human cDNA sequenc
C 575	16	2.6	1984	22	AAH16379	Human cDNA sequenc
C 576	16	2.6	2000	24	AB215631	Arabidopsis thalia
C 577	16	2.6	2000	24	AB215612	Arabidopsis thalia
C 578	16	2.6	2000	24	AB216728	Arabidopsis thalia
C 579	16	2.6	2000	24	AB217261	Arabidopsis thalia
C 580	16	2.6	2017	24	ABK51972	Rice config encodi
C 581	16	2.6	2017	25	ABX93208	DNA encoding rice
C 582	16	2.6	2025	21	AA544115	Arabidopsis thalia
C 583	16	2.6	2043	22	AAK94655	Human full-length
C 584	16	2.6	2093	21	AAK57996	2093 bp Candida al
C 585	16	2.6	2100	24	AAK57941	Human Stat2 protei
C 586	16	2.6	2100	24	AA158654	Human polynucleoti
C 587	16	2.6	2102	24	AB235779	Human HGF polynuci
C 588	16	2.6	2102	24	ABX10022	Human HGF DNA frag
C 589	16	2.6	2102	24	ABV78203	Human polynucleoti
C 590	16	2.6	2102	24	AB191744	Human polynucleoti
C 591	16	2.6	2104	23	AB126490	Drosophila melanog
C 592	16	2.6	2111	24	AAK24387	Human RNA metaboli
C 593	16	2.6	2113	22	AAH16488	Human cDNA sequenc
C 594	16	2.6	2128	22	AAK94169	Human full-length
C 595	16	2.6	2140	21	AAZ46161	cDNA sequence enco
C 596	16	2.6	2141	22	AAK46489	Novel protein kina
C 597	16	2.6	2142	22	ABN66993	Streptococcus poly
C 598	16	2.6	2142	24	ABN70353	Human polynucleoti
C 599	16	2.6	2159	22	AAK51803	Human cDNA sequenc
C 600	16	2.6	2162	22	AAH17641	Human polynucleoti
C 601	16	2.6	2172	14	AAV61952	Nucleotide sequenc
C 602	16	2.6	2173	14	AAQ37308	Encodes haematopo
C 603	16	2.6	2174	23	AB102215	Drosophila melanog
C 604	16	2.6	2178	24	AB157760	Canine hepatocyte
C 605	16	2.6	2182	24	AB551816	Novel human thromb
C 606	16	2.6	2184	13	AAQ20049	Human hepatocyte g
C 607	16	2.6	2184	13	AAQ26052	Human HGF. Homo s
C 608	16	2.6	2184	15	AAQ46040	Hepatocyte growth
C 609	16	2.6	2184	15	AAQ65137	Hepatocyte growth
C 610	16	2.6	2184	22	AAK91881	Human secreted pro
C 611	16	2.6	2187	12	AAQ10489	Hepatic parenchyma
C 612	16	2.6	2187	12	AAQ12399	Human hepatocyte g
C 613	16	2.6	2187	13	AAQ22146	Complete human HGF
C 614	16	2.6	2187	14	AAQ47832	Competative inhibi
C 615	16	2.6	2187	14	AAQ47833	Competative inhibi
C 616	16	2.6	2187	14	AAQ45702	Vascular endotheli
C 617	16	2.6	2187	19	AAV20546	Nucleic acid encod
C 618	16	2.6	2187	20	AAK87676	Human hepatocyte g
C 619	16	2.6	2187	22	AAH44781	Human polynucleoti
C 620	16	2.6	2188	22	AAK52516	Human hepatocyte g
C 621	16	2.6	2190	20	AAK87676	HGF-WSP hybrid pro
C 622	16	2.6	2190	20	AAK87677	HGF-WSP hybrid pro
C 623	16	2.6	2193	24	AB157559	Canine hepatocyte
C 624	16	2.6	2194	22	AAQ05150	Human secreted pro
C 625	16	2.6	2199	12	AAQ15177	Human leukocyte-de
C 626	16	2.6	2199	12	AAV53627	Human leukocyte-de
C 627	16	2.6	2208	25	AB114994	Pathogen specific
C 628	16	2.6	2211	23	AA568649	DNA encoding novel
C 629	16	2.6	2214	12	AAQ15176	Human leukocyte-de
C 630	16	2.6	2214	19	AAV53626	Human leukocyte-de
C 631	16	2.6	2214	25	AAV51053	Human DME-12 cDNA
C 632	16	2.6	2221	22	AAK52787	Human polynucleoti
C 633	16	2.6	2233	24	AB570484	Human bone remodel
C 634	16	2.6	2262	22	AA159434	Human polynucleoti
C 635	16	2.6	2262	22	AA161220	Human polynucleoti
C 636	16	2.6	2271	22	AA192551	Human polynucleoti
C 637	16	2.6	2281	22	AAK94167	Human full-length
C 638	16	2.6	2289	11	AAQ06088	Tumour cytotoxic f
C 639	16	2.6	2289	13	AAQ21066	TCF II-encoding se
C 640	16	2.6	2336	23	AB102217	Drosophila melanog
C 641	16	2.6	2393	12	AAQ14038	Human hepatocyte g
C 642	16	2.6	2394	13	AAQ22143	Human HGF gene par
C 643	16	2.6	2395	12	AAQ12397	Human hepatocyte g
C 644	16	2.6	2395	22	AAH44783	Hepatocyte growth
C 645	16	2.6	2422	21	AAK76578	Human ORFX ORP133
C 646	16	2.6	2469	24	AB156208	Human second RNA p
C 647	16	2.6	2473	22	ABK20648	Human nervous syst
C 648	16	2.6	2473	22	AA541698	Genomic sequence #
C 649	16	2.6	2495	23	AB189952	Drosophila melanog
C 650	16	2.6	2525	23	AB103282	Drosophila melanog
C 651	16	2.6	2530	22	AA135967	Human musculoskele
C 652	16	2.6	2530	25	ABK58955	cDNA encoding nove
C 653	16	2.6	2550	22	AAH18545	Human cDNA sequenc
C 654	16	2.6	2558	22	AAH17618	Human cDNA sequenc
C 655	16	2.6	2568	20	AAK84329	Stealth virus nucl
C 656	16	2.6	2574	24	AB232570	Candida albicans e
C 657	16	2.6	2592	22	AA160440	Human polynucleoti
C 658	16	2.6	2603	22	AAH13930	Human cDNA sequenc
C 659	16	2.6	2623	25	AB237537	5-phosphatase 12.7
C 660	16	2.6	2628	24	AB232128	Candida albicans e
C 661	16	2.6	2633	24	ABO70829	Listeria monocytog
C 662	16	2.6	2640	25	AB236098	Human secretory po
C 663	16	2.6	2687	24	ABK11593	C. diphteriae gen
C 664	16	2.6	2727	22	AAH14454	Human cDNA sequenc
C 665	16	2.6	2741	18	AA196844	Intron 14 of human

C 666	16	2.6	2758	24	ABN99426	Human secreted pro
C 667	16	2.6	2775	23	ABL20701	Drosophila melanog
C 668	16	2.6	2791	23	ABO70805	Listeria monocytog
C 669	16	2.6	2795	23	ABLI6644	Drosophila melanog
C 670	16	2.6	2816	21	AAK60049	Human secreted pro
C 671	16	2.6	2818	20	AAK87710	Human Burkitt's ly
C 672	16	2.6	2824	25	ABZ42633	Human CXC chemokin
C 673	16	2.6	2969	22	AAI66551	Human iron-sulphur
C 674	16	2.6	3011	22	AAH72579	Human cervical can
C 675	16	2.6	3011	24	AAK94899	Human DNA sequence
C 676	16	2.6	3108	24	ABO84185	Human P structural
C 677	16	2.6	3178	20	AAK99865	Human secreted pro
C 678	16	2.6	3178	22	AAK59289	Human CDNA encodin
C 679	16	2.6	3178	24	ABA90958	Human polynucleoti
C 680	16	2.6	3202	24	ABK69861	Human secreted pro
C 681	16	2.6	3220	23	ABLI30318	Drosophila melanog
C 682	16	2.6	3287	23	ABLI2554	Drosophila melanog
C 683	16	2.6	3301	24	ABV78035	Human polynucleoti
C 684	16	2.6	3309	24	ABV78035	Hypoxia-regulated
C 685	16	2.6	3316	21	AAK68344	DNA sequence assoc
C 686	16	2.6	3327	25	ACC46115	Human dihyb enzyme
C 687	16	2.6	3361	22	AAI36251	Human musculocele
C 688	16	2.6	3361	25	ABK59239	CDNA encoding nove
C 689	16	2.6	3378	23	ABLI20008	Drosophila melanog
C 690	16	2.6	3381	22	AAI02709	Human reproductive
C 691	16	2.6	3421	18	AAV74648	Staphylococcus aur
C 692	16	2.6	3432	25	ABZ10068	Haematopoietic cel
C 693	16	2.6	3432	25	ABZ10214	Haematopoietic cel
C 694	16	2.6	3473	22	AAH16188	Human CDNA sequenc
C 695	16	2.6	3495	20	AAK33814	Coding sequence fo
C 696	16	2.6	3496	24	ABLI61086	RNA uncouling enzy
C 697	16	2.6	3517	22	AAK80466	Human immune/haema
C 698	16	2.6	3543	23	ABLI24436	Drosophila melanog
C 699	16	2.6	3590	23	ABZ20174	Drosophila melanog
C 700	16	2.6	3599	24	AAK594825	Human DNA sequence
C 701	16	2.6	3620	22	ABN09117	Human Burkitt lymph
C 702	16	2.6	3649	22	ABD05122	Human secreted pro
C 703	16	2.6	3714	24	ABK83664	Human CDNA differe
C 704	16	2.6	3714	24	ABK83664	Gene LBR different
C 705	16	2.6	3731	22	AAK57140	DNA encoding Dros
C 706	16	2.6	3731	23	ABLI14332	Drosophila melanog
C 707	16	2.6	3759	23	AAK76295	DNA encoding novel
C 708	16	2.6	3795	20	AAK25348	Mouse DRM nucleoti
C 709	16	2.6	3825	22	AAH54430	S. epidermidis gen
C 710	16	2.6	3825	23	ABLI19976	Drosophila melanog
C 711	16	2.6	3842	23	ABO20700	Drosophila melanog
C 712	16	2.6	3855	12	AAQ13387	P.dentificans ge
C 713	16	2.6	3942	21	AAK99550	Nucleic acid sequ
C 714	16	2.6	3968	21	AAK68342	Rat insulin recept
C 715	16	2.6	3996	23	ABO03980	Drosophila melanog
C 716	16	2.6	4000	22	AAK86363	Human immune/haema
C 717	16	2.6	4001	22	AAK86364	Human immune/haema
C 718	16	2.6	4009	23	ABV24929	Human immune/haema
C 719	16	2.6	4009	23	ABV25228	Human prostate exp
C 720	16	2.6	4017	23	AAK83768	DNA encoding novel
C 721	16	2.6	4020	22	AAI06054	Human reproductive
C 722	16	2.6	4077	22	AAH18537	Human testicular a
C 723	16	2.6	4077	22	AAH18537	Human CDNA sequenc
C 724	16	2.6	4214	22	AAK72317	Human immune/haema
C 725	16	2.6	4358	22	AAK68397	Human immune/haema
C 726	16	2.6	4359	23	AAK78986	DNA encoding novel
C 727	16	2.6	4380	23	ABLI28156	Drosophila melanog
C 728	16	2.6	4504	23	ABLI05226	Drosophila melanog
C 729	16	2.6	4528	22	AAH26937	Trichoderma reesei
C 730	16	2.6	4528	24	AAH26937	Trichoderma reesei
C 731	16	2.6	4602	23	ABLI1382	Drosophila melanog
C 732	16	2.6	4609	22	AAK26889	Beet necrotic yell
C 733	16	2.6	4661	24	ABQ67021	Human angiogenesis
C 734	16	2.6	4761	23	ABLI14956	Drosophila melanog
C 735	16	2.6	4845	23	ABLI20700	Drosophila melanog
C 736	16	2.6	4896	24	AAH43974	Bacillus thuringie
C 737	16	2.6	4976	23	ABLI07312	Drosophila melanog
C 738	16	2.6	5040	20	AAK20272	Borrelia burgdorfe
C 739	16	2.6	5046	22	AAH48716	T. thermophila tri
C 740	16	2.6	5075	23	ABLI30321	Drosophila melanog
C 741	16	2.6	5099	24	AAH29643	Arabidopsis thalia
C 742	16	2.6	5099	24	ABK91396	Arabidopsis thalis
C 743	16	2.6	5160	21	AAK21033	Human low adenosin
C 744	16	2.6	5160	21	AAA43911	Human adenosine re
C 745	16	2.6	5160	24	ABK84262	Human CDNA differe
C 746	16	2.6	5183	22	AAK45506	Chemically pretrea
C 747	16	2.6	5183	24	ABLI3349	Human immune syste
C 748	16	2.6	5183	24	ABK28438	DNA transcription
C 749	16	2.6	5185	24	ABLI3034	Human immune syste
C 750	16	2.6	5221	24	ABLI3914	Human immune syste
C 751	16	2.6	5236	24	ABLI32350	Human immune syste
C 752	16	2.6	5299	22	AAK57120	DNA encoding Dros
C 753	16	2.6	5299	23	ABLI2080	Drosophila melanog
C 754	16	2.6	5303	24	ABLI3870	Human immune syste
C 755	16	2.6	5332	23	ABLI12460	Drosophila melanog
C 756	16	2.6	5356	24	ABLI70441	Chemically treated
C 757	16	2.6	5460	22	ABLI33904	Human immune syste
C 758	16	2.6	5506	22	AAK69689	Human immune/haema
C 759	16	2.6	5728	24	ABK34472	Human immune syste
C 760	16	2.6	5769	24	ABQ70951	Signal transductio
C 761	16	2.6	5771	24	ABLI33951	Listeria monocytog
C 762	16	2.6	5798	24	ABO67012	Human immune syste
C 763	16	2.6	5798	24	ABLI32169	Human angiogenesis
C 764	16	2.6	5844	24	ABLI49390	Human immune syste
C 765	16	2.6	5855	20	AAI13042	Human polynucleoti
C 766	16	2.6	5855	24	ABK98837	Enterococcus faeca
C 767	16	2.6	5898	24	ABN97213	Enterococcus faeca
C 768	16	2.6	5942	24	ABLI70534	Gene #3711 used to
C 769	16	2.6	5942	24	ABK33945	Chemically treated
C 770	16	2.6	5942	24	AAK61135	Human DNA for stag
C 771	16	2.6	5942	24	ABK31223	Human gene regulat
C 772	16	2.6	5942	25	ABZ10002	Signal transductio
C 773	16	2.6	5942	25	ABZ10088	Haematopoietic cel
C 774	16	2.6	5942	25	ABZ10148	Haematopoietic cel
C 775	16	2.6	5942	25	ABZ10234	Haematopoietic cel
C 776	16	2.6	5945	24	ABLI32084	Human immune syste
C 777	16	2.6	5958	24	ABLI3059	Human immune syste
C 778	16	2.6	5962	24	ABLI3468	Human immune syste
C 779	16	2.6	5990	22	AAK67673	Human immune syste
C 780	16	2.6	5999	24	ABLI2853	Human immune/haema
C 781	16	2.6	5999	24	ABK28192	DNA transcription
C 782	16	2.6	6000	24	AAK28999	Bugula neritina PK
C 783	16	2.6	6030	24	AAK61347	Human gene regulat
C 784	16	2.6	6030	24	ABK28311	DNA transcription
C 785	16	2.6	6048	24	ABLI4031	Human immune syste
C 786	16	2.6	6048	24	AAK53353	Chemically pretrea
C 787	16	2.6	6062	24	ABLI4079	Human immune syste
C 788	16	2.6	6072	24	ABLI2030	Human immune syste
C 789	16	2.6	6076	24	ABK28347	DNA transcription
C 790	16	2.6	6083	22	AAK46714	Tumour suppressor
C 791	16	2.6	6092	24	AAK61080	Human gene regulat
C 792	16	2.6	6115	24	ABLI3801	Human immune syste
C 793	16	2.6	6134	22	AAI169936	CDNA encoding nove
C 794	16	2.6	6134	25	ABK59924	Human immune syste
C 795	16	2.6	6151	24	ABLI3610	DNA transcription
C 796	16	2.6	6151	24	ABK28275	Human immune syste
C 797	16	2.6	6154	24	ABLI70167	Chemically treated
C 798	16	2.6	6154	24	AAK61112	Human gene regulat
C 799	16	2.6	6164	24	ABK31200	Signal transductio
C 800	16	2.6	6171	24	ABLI2039	Human immune syste
C 801	16	2.6	6182	24	ABLI33011	Human immune syste
C 802	16	2.6	6182	24	ABLI34014	Human immune syste
C 803	16	2.6	6187	23	ABLI24052	Drosophila melanog
C 804	16	2.6	6230	23	ABLI22216	Drosophila melanog
C 805	16	2.6	6274	24	ABK36110	CDNA sequence #501
C 806	16	2.6	6277	22	AAK46728	Tumour suppressor
C 807	16	2.6	6277	22	ABLI34040	Human immune syste
C 808	16	2.6	6285	20	AAI13352	Enterococcus faeca
C 809	16	2.6	6285	24	ABK99147	Enterococcus faeca
C 810	16	2.6	6342	23	ABLI5592	Drosophila melanog
C 811	16	2.6	6396	24	ABLI34247	Human immune syste

812	16	2.6	6418	24	ABL32323	Human immune syste	C 885	16	2.6	9481	22	ABA20646	Human nervous syst
813	16	2.6	6418	24	AAS61074	Human gene regulat	C 886	16	2.6	9481	22	AAS41696	Genomic sequence #
814	16	2.6	6428	22	AAK78562	Human immune/haema	C 887	16	2.6	9656	22	AAS41696	Tumour suppressor
815	16	2.6	6431	24	ABO67120	Human angiogenesis	C 888	16+	2.6	9656	22	ABN80213	Human chemically m
816	16	2.6	6432	22	AAS46558	Tumour suppressor	C 889	16	2.6	9722	22	ABA15166	Human nervous syst
817	16	2.6	6534	24	ABL32471	Human immune syste	C 890	16	2.6	9848	23	ABL10538	Drosophila melanog
818	16	2.6	6544	22	AAS45341	Chemically pretrea	C 891	16	2.6	9876	24	ABL12093	Human immune syste
819	16	2.6	6544	24	ABL32647	Human immune syste	C 892	16	2.6	9885	23	ABL16338	Drosophila melanog
820	16	2.6	6558	23	ABL12566	Drosophila melanog	C 893	16	2.6	9889	23	ABL07368	Drosophila melanog
821	16	2.6	6565	22	AAS46466	Tumour suppressor	C 894	16	2.6	9929	22	ABA17906	Human nervous syst
822	16	2.6	6565	22	ABL31327	Signal transductio	C 895	16	2.6	10090	23	ABL10760	Drosophila melanog
823	16	2.6	6609	24	ABN80246	Human chemically m	C 896	16	2.6	10100	23	ABL29778	Drosophila melanog
824	16	2.6	6609	24	ABL33882	Human immune syste	C 897	16	2.6	10115	24	ABK90052	Human GSP3 genom
825	16	2.6	6631	24	ABN28339	DNA transcription	C 898	16	2.6	10317	23	ABL24598	Drosophila melanog
826	16	2.6	6699	24	ABN80183	Human chemically m	C 899	16	2.6	10377	22	ABL44220	Human immune syste
827	16	2.6	6774	24	ABO67155	Human angiogenesis	C 900	16	2.6	10503	22	AAK89097	Human digestive sy
828	16	2.6	6904	24	ABL32212	Human immune syste	C 901	16	2.6	11036	20	AAK13401	Enterococcus faeca
829	16	2.6	6933	23	ABL07454	Drosophila melanog	C 902	16	2.6	11036	24	ABS99196	Enterococcus faeca
830	16	2.6	6935	24	ABL92263	Chemically treated	C 903	16	2.6	11115	22	AAS41967	Genomic sequence #
831	16	2.6	6980	24	ABL32453	Human immune syste	C 904	16	2.6	11115	22	AAS41974	Genomic sequence #
832	16	2.6	7008	22	AAS46531	Tumour suppressor	C 905	16	2.6	11115	23	ABK72139	Human ovarian anti
833	16	2.6	7113	24	ABL32805	Human immune syste	C 906	16	2.6	11115	24	ABK91731	Novel ovarian rela
834	16	2.6	7114	22	AAK70622	Human immune/haema	C 907	16	2.6	11209	24	ABN80137	Human chemically m
835	16	2.6	7115	22	AAK07153	Human reproductive	C 908	16	2.6	11456	22	AAK69400	Human immune/haema
836	16	2.6	7167	24	ABL32400	Human immune syste	C 909	16	2.6	11944	22	AAK69400	Signal transductio
837	16	2.6	7306	24	ABO67109	Human angiogenesis	C 910	16	2.6	11907	24	ABL34187	Human immune syste
838	16	2.6	7341	24	ABL33636	Human angiogenesis	C 911	16	2.6	12000	24	ABK34015	Human DNA for stag
839	16	2.6	7353	24	ABL33073	Human immune syste	C 912	16	2.6	12133	24	ABN80322	Human chemically m
840	16	2.6	7353	24	AAD28363	Human chemically t	C 913	16	2.6	12237	24	ABL34358	Human immune syste
841	16	2.6	7355	24	ABN80296	Human chemically m	C 914	16	2.6	12507	24	ABL32298	Human immune syste
842	16	2.6	7403	22	AAS46803	Tumour suppressor	C 915	16	2.6	12693	22	ABA20625	Human nervous syst
843	16	2.6	7403	22	AAS46804	Tumour suppressor	C 916	16	2.6	12693	22	AAK79994	Human immune/haema
844	16	2.6	7403	24	ABL34216	Human immune syste	C 917	16	2.6	12808	23	ABL30320	Drosophila melanog
845	16	2.6	7403	24	ABL34217	Human immune syste	C 918	16	2.6	13103	23	ABL29868	Drosophila melanog
846	16	2.6	7500	24	ABL33115	Human immune syste	C 919	16	2.6	13111	23	ABL13364	Drosophila melanog
847	16	2.6	7503	24	ABO67009	Human angiogenesis	C 920	16	2.6	13123	24	ABL54364	Chemically treated
848	16	2.6	7503	24	ABL33548	Human immune syste	C 921	16	2.6	13123	24	ABK31423	Signal transductio
849	16	2.6	7577	23	ABL02214	Drosophila melanog	C 922	16	2.6	13125	24	ABL70283	Chemically treated
850	16	2.6	7577	12	AAO15133	Zucchini ACC synth	C 923	16	2.6	13125	24	ABL33226	Human immune syste
851	16	2.6	7587	19	AAV15703	Zucchini ACC synth	C 924	16	2.6	13125	24	ABL4556	Human metastasis a
852	16	2.6	7587	22	AAD04543	Zucchini CP-ACC 1B	C 925	16	2.6	13361	23	ABL17960	Drosophila melanog
853	16	2.6	7587	22	AAF23620	Zucchini ACC synth	C 926	16	2.6	13395	22	AAK74325	Human immune/haema
854	16	2.6	7676	24	ABL70409	Chemically treated	C 927	16	2.6	13444	23	ABL15546	Drosophila melanog
855	16	2.6	7676	24	ABL34598	Human metastasis a	C 928	16	2.6	13491	23	ABL25572	Drosophila melanog
856	16	2.6	7793	25	ABZ73859	Secreted protein g	C 929	16	2.6	13548	21	AAF21037	Human low adenosin
857	16	2.6	7793	25	ABZ7436	Human secreted pro	C 930	16	2.6	13548	21	AAA34915	Human adenosine re
858	16	2.6	7829	24	ABL70266	Chemically treated	C 931	16	2.6	13784	21	ABK40061	Human chemically p
859	16	2.6	7829	24	ABL33105	Human immune syste	C 932	16	2.6	13792	24	ABL33570	Human immune syste
860	16	2.6	7829	24	AAS61191	Human gene regulat	C 933	16	2.6	14316	24	ABL70606	Chemically treated
861	16	2.6	7829	24	ABK31287	Signal transductio	C 934	16	2.6	14316	24	AAS61445	Human gene regulat
862	16	2.6	7843	23	ABL28755	Drosophila melanog	C 935	16	2.6	14316	24	ABK31519	Signal transductio
863	16	2.6	7857	24	ABO67075	Human angiogenesis	C 936	16	2.6	14362	24	ABO67048	Human angiogenesis
864	16	2.6	7924	24	ABK40065	Human chemically p	C 937	16	2.6	14494	23	ABL17946	Drosophila melanog
865	16	2.6	7924	24	ABL34138	Human immune syste	C 938	16	2.6	14617	22	ABA19132	Human nervous syst
866	16	2.6	8032	24	ABL70447	Chemically treated	C 939	16	2.6	14627	22	ABA19130	Human nervous syst
867	16	2.6	8032	24	AAS61408	Human gene regulat	C 940	16	2.6	14708	22	AAS45514	Chemically pretrea
868	16	2.6	8032	24	ABK31478	Signal transductio	C 941	16	2.6	14708	24	ABL92325	Chemically treated
869	16	2.6	8115	22	AAS41935	Genomic sequence #	C 942	16	2.6	14708	24	ABL34245	Human immune syste
870	16	2.6	8115	22	AAS41947	Genomic sequence #	C 943	16	2.6	14708	24	ABK28450	DNA transcription
871	16	2.6	8115	22	AAS41961	Genomic sequence #	C 944	16	2.6	14855	22	ABA15164	Human nervous syst
872	16	2.6	8115	22	AAS41963	Genomic sequence #	C 945	16	2.6	15247	24	ABK40064	Human chemically p
873	16	2.6	8166	24	ABL33792	Human immune syste	C 946	16	2.6	15247	24	ABL4083	Human immune syste
874	16	2.6	8237	22	AAS46802	Tumour suppressor	C 947	16	2.6	15396	23	ABL7860	Drosophila melanog
875	16	2.6	8298	24	ABN80190	Human chemically m	C 948	16	2.6	15643	22	AAS31559	Human DNA for a no
876	16	2.6	8486	24	ABL34445	Human immune syste	C 949	16	2.6	15643	22	ABO66883	Human polynucleoti
877	16	2.6	8559	22	AAI199011	Human excretory re	C 950	16	2.6	15732	22	AAS45388	Chemically pretrea
878	16	2.6	8559	22	AAI63361	Human kidney relat	C 951	16	2.6	15732	24	ABK28233	DNA transcription
879	16	2.6	9000	24	ABK70903	Mouse HYPLIP1 geno	C 952	16	2.6	15743	24	ABK28396	DNA transcription
880	16	2.6	9084	24	ABK48677	Genomic DNA sequen	C 953	16	2.6	15872	22	AAS46520	Tumour suppressor
881	16	2.6	9157	24	ABL33605	Human immune syste	C 954	16	2.6	16084	22	AAI36151	Human muscle skele
882	16	2.6	9157	24	ABL33500	Human immune syste	C 955	16	2.6	16084	25	ABK59149	CDNA encoding nove
883	16	2.6	9206	24	ABL33674	Human immune syste	C 956	16	2.6	16896	23	ABL20462	Drosophila melanog
884	16	2.6	9345	21	AAZ93966	Mouse utromodulin p	C 957	16	2.6	16914	24	ABL70315	Chemically treated

C 958	16	2.6	16914	24	AA561253	Human gene regulat
C 959	16	2.6	17656	24	AB555502	Sweetgum Aganous g
C 960	16	2.6	17721	24	AB133728	Human immune syste
C 961	16	2.6	17738	24	AB133539	Human immune syste
C 962	16	2.6	17869	24	ABK39921	Human chemically p
C 963	16	2.6	17869	24	ABJ32105	Human immune syste
C 964	16	2.6	18011	24	ABJ32035	Human immune syste
C 965	16	2.6	18047	22	AAK80292	Human immune/haema
C 966	16	2.6	19011	22	AA103125	Human reproductive
C 967	16	2.6	19011	22	AA103126	Human reproductive
C 968	16	2.6	19011	22	AAK84511	Human immune/haema
C 969	16	2.6	19011	22	AAK84512	Human immune/haema
C 970	16	2.6	19082	24	ABJ32626	Human immune syste
C 971	16	2.6	19236	24	ABN80226	Human chemically m
C 972	16	2.6	19659	22	AAK65309	Human immune/haema
C 973	16	2.6	20598	22	AA244851	Nucleotide sequenc
C 974	16	2.6	20598	24	AA242515	Human zaiplna3 gen
C 975	16	2.6	20746	22	AA107353	Human reproductive
C 976	16	2.6	21354	22	AA546784	Tumour suppressor
C 977	16	2.6	21354	22	AA546786	Tumour suppressor
C 978	16	2.6	22028	24	ABA933286	Human acetyl-Coenz
C 979	16	2.6	22028	24	ABA933288	Human acetyl-Coenz
C 980	16	2.6	23203	23	AB117834	Drosophila melanog
C 981	16	2.6	24939	22	AAK65622	Human immune/haema
C 982	16	2.6	25002	24	ABQ74278	C. elegans Z92825
C 983	16	2.6	25423	22	AAK90279	Human digestive sy
C 984	16	2.6	25423	22	AA157656	Human colorectal c
C 985	16	2.6	25423	24	AB599833	Genomic DNA #37 en
C 986	16	2.6	25424	22	AAK90280	Human digestive sy
C 987	16	2.6	25424	22	AA157657	Human colorectal c
C 988	16	2.6	25424	24	AB599834	Genomic DNA #38 en
C 989	16	2.6	25911	23	AB102604	Drosophila melanog
C 990	16	2.6	25929	23	AB102602	Drosophila melanog
C 991	16	2.6	26016	19	AAV57272	Human flavin-conta
C 992	16	2.6	26456	22	AB119696	Human nervous syst
C 993	16	2.6	27571	22	AB119222	Human nervous syst
C 994	16	2.6	27572	22	AB119221	Human nervous syst
C 995	16	2.6	28001	24	AB554410	Human hydroxymethy
C 996	16	2.6	28001	25	ABK93300	Gene encoding huma
C 997	16	2.6	28313	22	AA136829	Human musculoskele
C 998	16	2.6	28313	25	AAK59817	cDNA encoding nove
C 999	16	2.6	28432	23	AB105010	Drosophila melanog
C 1000	16	2.6	28506	24	ABK90191	Human flavin conta

ALIGNMENTS

RESULT 1
ID ABK97884 standard; DNA; 622 BP.

XX ABK97884;

10-OCT-2002 (first entry)

DE DNA encoding Lawsonia intracellularis antigenic flhB protein.

XX Immunogen; flhB; flhR; ntrC; glhH; motA; motB; clyC; yfW; yfN;
XX porcine; pig; avian; bird; porcine proliferative enteropathy; PPE;
XX intestinal adenomatosis complex; porcine intestinal adenomatosis;
XX PIA; necrotic enteritis; proliferative haemorrhagic enteropathy;
XX regional ileitis; haemorrhagic bowel syndrome; vaccine; antibacterial;
XX porcine proliferative enteritis; Campylobacter spp.-induced enteritis;
XX gene; de.

OS Lawsonia intracellularis.

PN WO200238594-A1.

XX 16-MAY-2002.

PF 09-NOV-2001; 2001WO-AU01462.

XX 10-NOV-2000; 2000AU-0001381.
PR 17-NOV-2000; 2000US-249596P.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AUPO-) AUSTRALIAN PORK LTD.
PA (PFIZ) PFIZER PROD INC.
PI Rosey EL, King KW, Good RT, Strugnell RA;
DR WPI, 2002-557448/59.
DR P-PSDB; ABG68910.

PT New immunogenic polypeptide comprising epitope of Lawsonia spp.
PT polypeptide such as flhB, flhR, ntrC, glhH, motA, polypolypates, useful
PT in vaccines for treatment of porcine proliferative enteropathy in pigs
PT and birds

PS Claim 6; Page 99-100; 155pp; English.

XX The invention describes an isolated or recombinant immunogenic
CC polypeptide (I) which comprises, mimics or cross-reacts with a B-cell or
CC T-cell epitope of a Lawsonia spp. polypeptide such as flhB, flhR, ntrC,
CC glhH, motA, motB, clyC, yfW or yfN polypeptides. (I) is useful for
CC identifying whether or not a porcine or avian animal has suffered from a
CC past infection, or is currently infected, with Lawsonia spp. or a
CC microorganism that is immunologically cross-reactive with Lawsonia spp.
CC Antibodies are useful for diagnosing infection of a porcine or avian
CC animal by Lawsonia spp. or a microorganism that is immunologically
CC cross-reactive with Lawsonia spp.. A nucleic acid encoding a Lawsonia
CC spp. immunogen is useful as probes or primers for detecting Lawsonia spp.
CC or related microorganism in a biological sample derived from a porcine or
CC avian animal subject. (I) is preferably useful for vaccinating porcine
CC animals against intestinal diseases collectively known as porcine
CC proliferative enteropathy (PPE), previously known as intestinal
CC adenomatosis complex, porcine intestinal adenomatosis (PIA), necrotic
CC enteritis, proliferative haemorrhagic enteropathy, regional ileitis,
CC haemorrhagic bowel syndrome, porcine proliferative enteritis and
CC Campylobacter spp.-induced enteritis. (I) is also useful in vaccines for
CC the prophylaxis and treatment of PPE in birds. This sequence encodes a
CC Lawsonia intracellularis immunogenic peptide used in the creation of a
CC porcine vaccine described in the invention.

SQ Sequence 622 BP; 189 A; 92 C; 123 G; 218 T; 0 other;

Query Match 100.0%; Score 622; DB 24; Length 622;
Best Local Similarity. 100.0%; Pred. No. 1.5e-252;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCTGATGATCCAGTAAACAGAGAAGCAACCCGGAACGACGTACAGAGCTCGT	60
DB	1	ATGCTGATGATCCAGTAAACAGAGAAGCAACCCGGAACGACGTACAGAGCTCGT	60
QY	61	TCTGAAGGAGTGTCCCTAAATCAGAGAAGGTTACTAAGACATTGACTGCACAGAG	120
DB	61	TCTGAAGGAGTGTCCCTAAATCAGAGAAGGTTACTAAGACATTGACTGCACAGAG	120
QY	121	ATGCTGGGCGCTTCTATTATTACAGCGGTAAATGGAGCTCATTTTGAACAATTTTCTAC	180
DB	121	ATGCTGGGCGCTTCTATTATTACAGCGGTAAATGGAGCTCATTTTGAACAATTTTCTAC	180
QY	181	TATATTTTACAGATCATTTCCGTTGAGGTTACAGACAGTCAAGTATATCTTATTT	240
DB	181	TATATTTTACAGATCATTTCCGTTGAGGTTACAGACAGTCAAGTATATCTTATTT	240
QY	241	ATTATGTTGCTCAAGATAGCTATTTATGATGCCAATATTAATCTTTATGCTGTT	300
DB	241	ATTATGTTGCTCAAGATAGCTATTTATGATGCCAATATTAATCTTTATGCTGTT	300
QY	301	ACGGATGATTTTCAATTCGTGTACAGTGTGTCATTTATGACTACAAAGTTTAA	360
DB	301	ACGGATGATTTTCAATTCGTGTACAGTGTGTCATTTATGACTACAAAGTTTAA	360


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QY 361 TTTAAATGAGTAATTTATATATATAAAGGTTGAAGAGATGTTGCTTCAACAA 420
DB 361 TTTAAATGAGTAATTTATATATATAAAGGTTGAAGAGATGTTGCTTCAACAA 420
QY 421 ACACCTTGTCAGCTTTACGTAAGTTTACGTAAGTAATTTGTATAGTATTTGTCATAT 480
DB 421 ACACCTTGTCAGCTTTACGTAAGTTTACGTAAGTAATTTGTATAGTATTTGTCATAT 480
QY 481 ATGATTTAAAGAGAGAGATTTTCAAACTTTTACCATTAATATATGCAAGTCTTCAGGT 540
DB 481 ATGATTTAAAGAGAGAGATTTTCAAACTTTTACCATTAATATATGCAAGTCTTCAGGT 540
QY 541 GTGGCAGATTATATGCTTAATATACAGAAATGACTTTTATATACGTAATTCCTATG 600
DB 541 GTGGCAGATTATATGCTTAATATACAGAAATGACTTTTATATACGTAATTCCTATG 600
QY 601 ACAATTATTGCAATCGGAGATC 622
DB 601 ACAATTATTGCAATCGGAGATC 622

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RESULT 2

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ABV96020/C
ID ABV96020 standard; cDNA; 340 BP.
XX
AC ABV96020;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 1428.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
XX cytosolic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US02781.
XX
PR 30-JAN-2001; 2001US-265305P.
XX
PR 31-JAN-2001; 2001US-265682P.
XX
PR 09-FEB-2001; 2001US-267568P.
XX
PR 21-MAR-2001; 2001US-278651P.
XX
PR 28-APR-2001; 2001US-287112P.
XX
PR 16-MAY-2001; 2001US-291631P.
XX
PR 12-JUL-2001; 2001US-305484P.
XX
PR 20-AUG-2001; 2001US-313999P.
XX
PR 27-NOV-2001; 2001US-333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX
DR
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful
XX for diagnosing, preventing and/or treating cancer, particularly
XX pancreatic cancer -
XX
PS Claim 1; SEQ ID NO 1428; 300pp + Sequence Listing; English.
XX
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
CC (b) complements of (a); (c) sequences consisting of at least 20
CC contiguous residues of (a); (d) sequences that hybridize to (a), under
CC moderately stringent conditions; (e) sequences having at least 75% or 90%
CC identity to (a), or (f) degenerate variants of (a). Polypeptides
CC (ABP6556-ABP6837) encoded by (I) and oligonucleotide comprising polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations and
CC

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CC antigen presenting cells expressing the polypeptide are useful in
CC treating pancreatic cancer and stimulating an immune response. The
CC polynucleotide can be used as probes or primers for nucleic acid
CC hybridisation, in the design and preparation of ribozyme molecules for
CC inhibiting expression of the tumour polypeptides and proteins in the
CC tumour cells, in vaccines and for gene therapy.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 340 BP; 100 A; 81 C; 64 G; 94 T; 1 other;

```

Query Match 3.1%; Score 19; DB 24; Length 340;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 261 AGCTATTTTATGATGCCA 279
DB .307 AGCTATTTTATGATGCCA 289

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RESULT 3

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ABA58347/C
ID ABA58347 standard; DNA; 390 BP.
XX
AC ABA58347;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #6652.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
DR
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX
PS Claim 1; SEQ ID NO 6652; 639pp + sequence listing; English.
XX
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

```

Query Match 3.1%; Score 19; DB 22; Length 390;

Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 ATATGCTTATTATTAT 246
Db 79 ATATGCTTATTATTAT 61

RESULT 4
ABA27469/c

ID ABA27469 standard; DNA; 390 BP.

AC ABA27469;

DT 23-JAN-2002 (first entry)

DE Probe #5935 for gene expression analysis in human heart cell sample.

KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX hearts -

XX Claim 1; SEQ ID No 5935; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

XX measuring human gene expression in a sample derived from human heart. The

XX present sequence is one such probe. The probes may be used for

XX predicting, measuring and displaying gene expression in samples derived

XX from the human heart via microarrays. By measuring gene expression, the

XX probes are useful for predicting, diagnosing, grading, staging,

XX monitoring and prognosing diseases of the human heart and vascular system

XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

XX congenital heart disease.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

RESULT 5
AAK06446/c

ID AAK06446 standard; DNA; 390 BP.

AC AAK06446;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe SEQ ID NO: 6437.

KW Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer; ss.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains -

XX Example 4; SEQ ID NO: 6437; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is one of the probes of the

XX invention.

XX Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

XX Query Match 3.1%; Score 19; DB 22; Length 390;

XX Best Local Similarity 100.0%; Pred. No. 37;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 ATATGCTTATTATTAT 246
Db 79 ATATGCTTATTATTAT 61

RESULT 6

AAK32124/c

ID AAK32124 standard; DNA; 390 BP.

AC AAK32124;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 6681.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukemia; lymphoma; myeloma; ss.

XX

```
OS Homo sapiens.
XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PN WO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 6681; 658bp + Sequence Listing; English.
XX
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukemia and myeloma. The present sequence is one of
XX the probes of the invention.
XX
XX SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

Query Match 3.1%; Score 19; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 228 ATATGCTTTATTTATTTAT 246
Db 79 ATATGCTTTATTTATTTAT 61

RESULT 7
AA115959/c
ID AA115959 standard; DNA; 390 BP.
XX
XX AA115959;
XX
XX 12-OCT-2001 (first entry)
XX
XX Probe #5892 for gene expression analysis in human cervical cell sample.
XX
XX Probe; human; microarray; gene expression; cervical epithelial cell;
XX cervical cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
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XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 25; SEQ ID No 5892; 487bp; English.
XX
XX CC The present invention relates to human single exon nucleic acid probes
XX (SENPs). The present sequence is one such probe. The SENPs are derived
XX from human Hela cells. The SENPs can be used to produce a single exon
XX microarray, which can be used for measuring human gene expression in a
XX sample derived from human cervical epithelial cells. By measuring gene
XX expression, the probes are therefore useful in grading and/or staging
XX of diseases of the cervix, notably cervical cancer.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

Query Match 3.1%; Score 19; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 228 ATATGCTTTATTTATTTAT 246
Db 79 ATATGCTTTATTTATTTAT 61

RESULT 8
AA137975/c
ID AA137975 standard; DNA; 390 BP.
XX
XX AA137975;
XX
XX 17-OCT-2001 (first entry)
XX
XX Probe #6661 used to measure gene expression in human placenta sample.
XX
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID No 6661; 654bp; English.
```

XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;
QY
Query Match 3.1%; Score 19; DB 22; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 228 ATATGCTTATTATTAT 246
79 ATATGCTTATTATTAT 61
RESULT 9
ID ABS31820/c
XX ABS31820 standard; DNA; 390 BP.
AC ABS31820;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 6810.
XX
KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00664.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488698/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analysing gene expression in human adult liver -
XX
XX Claim 1; SEQ ID No 6810; 658pp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (1) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult
XX liver. (1) may be used for predicting, measuring and displaying gene
XX expression in samples derived from human adult liver. The genes
XX identified may be involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
XX is associated with coronary heart disease. ABS25011-ABS51005 represent
XX human liver single exon nucleic acid probes of the invention.
XX Note: The sequence information for this patent does not appear in the
XX printed specification but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;
QY
Query Match 3.1%; Score 19; DB 23; Length 390;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 228 ATATGCTTATTATTAT 246
79 ATATGCTTATTATTAT 61
RESULT 10
ID ABS06891/c
XX ABS06891 standard; DNA; 390 BP.
AC ABS06891;
XX
XX 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe from lung SEQ ID No 6882.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease.
XX
XX Homo sapiens.
XX
XX WO200186003-A2.
XX
XX 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
XX
PR 26-MAY-2000; 2000US-207456P.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-234687P.
XX
PR 27-SEP-2000; 2000US-236359P.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples -
XX
XX Claim 1; SEQ ID No 6882; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12618 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX probes; the novel set of probes which hybridise at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression in a
XX sample derived from human lung, comprising (a) contacting the array with
XX a collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of
XX the array; identifying exons in a eukaryotic genome, comprising
XX (a) algorithmically predicting at least one exon from genomic sequences
XX of the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridization to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 1201 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karsenger syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 390 BP; 112 A; 120 C; 37 G; 121 T; 0 other;

CC Query Match 3.1%; Score 19; DB 24; Length 390;
CC Best Local Similarity 100.0%; Pred. No. 37;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 ATATGCTTATTATTAT 246
DB 79 ATATGCTTATTATTAT 61

DB 79 ATATGCTTATTATTAT 61

RESULT 11
ABN67186
ID ABN67186 standard; DNA; 693 BP.

AC ABN67186;

DT 01-JUN-2002 (first entry)

DE Streptococcus polymnucleotide SBQ ID NO 2285.

XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; Streptococcus pyogenes; antibacterial; gene;

XX antiinflammatory; infection; vaccine; meningitis; gene therapy; de.

OS Streptococcus pyogenes.

XX WO200234771-A2.

PD 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB04789.

PR 27-OCT-2000; 2000GB-0026333.

PR 24-NOV-2000; 2000GB-0028727.

PR 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX Telford J, Maignani V, Margarit Ros YI, Grandi G, Fraser C;

PI Tettelein H;

XX WPI, 2002-352536/38.

DR F-PSDB; ABP26555.

PT New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX Claim 7; Page 3379; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.

XX Sequence 693 BP; 193 A; 126 C; 171 G; 203 T; 0 other;

CC Query Match 3.1%; Score 19; DB 24; Length 693;
CC Best Local Similarity 100.0%; Pred. No. 37;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 TGATGCCAATATTACTTT 290
DB 603 TGATGCCAATATTACTTT 621

DB 603 TGATGCCAATATTACTTT 621

RESULT 12.
ACA04580
ID ACA04580 standard; cDNA; 948 BP.

AC ACA04580;

DT 28-MAY-2003 (first entry)

DE cDNA encoding human membrane associated protein fragment #28.

XX Human; ss; gene; microarray; membrane-associated protein; neuropathology;

KW immunopathology; pancreatic disease; cancer; diabetes; hyperlipidaemia;

KW pancreatic cholera; Alzheimer's disease; Huntington's disease; sarcoma;

KW fibrocystic disease; leukaemia; adenocarcinoma; AIDS; allergy; anaemia;

XX asthma; gout; dementia.

OS Homo sapiens.

XX US6492505-B1.

PD 10-DEC-2002.

XX 31-JAN-2000; 2000US-0495050.

PR 01-FEB-1999; 99US-118318P.

PA (INCY-) INCYTE GENOMICS INC.

XX Reddy R, Guegler KJ, Au-Young J;

PI WPI; 2003-327324/31.

XX Combination for research/diagnostic applications and for monitoring
PT treatment of e.g., cancer, comprises polynucleotides comprising a
PT fragment of gene encoding membrane-associated proteins, receptors or
PT ion channels -
XX Claim 1; Column 51-52; 147pp; English.

XX The invention relates to a combination comprising several polynucleotide
 CC sequences comprising a fragment of gene encoding membrane-associated
 CC proteins, receptors or ion channels. The combination is useful as a
 CC probe, for research and diagnostic applications, for monitoring the
 CC expression of several expressed polynucleotides, in the diagnosis and
 CC monitoring of treatment of pancreatic disease, cancer, immunopathology or
 CC neuropathology, for investigating an individual's predisposition to the
 CC above disease, in genetic or gene expression analysis of polynucleotide
 CC sequences, to investigate cellular responses to infection or drug
 CC treatment, as hybridizable array elements in a microarray, to purify a
 CC subpopulation of mRNAs, cDNAs or genomic fragments in a sample, in
 CC diagnostics, prognostics and treatment regimens, in drug discovery and
 CC development, in toxicological and carcinogenicity studies, and in
 CC forensics or pharmacogenomics, to monitor the progression of disease, to
 CC monitor the efficacy of treatment, to diagnose the conditions of the
 CC pancreas e.g. diabetes, pancreatic cholera, hyperlipidemia or
 CC fibrocystic disease, to diagnose a cancer e.g. leukemia, adenocarcinoma
 CC or sarcoma, to diagnose immunopathologies e.g. AIDS, allergies, anaemia,
 CC asthma or gout, to diagnose neuropathologies e.g. Alzheimer's disease,
 CC dementia or Huntington's disease, to rapidly screen large numbers of
 CC candidate drug molecules and as query sequences against GenBank,
 CC SwissProt, BLOCKS and PRINTS databases. The combination is employed to
 CC fine tune the treatment regimen and thus the expression patterns
 CC associated with undesirable side effects are avoided. The present
 CC sequence represents a cDNA encoding a fragment of gene encoding human
 CC membrane-associated proteins, receptors or ion channels.

XX SQ Sequence 948 BP; 291 A; 171 C; 194 G; 292 T; 0 other;

Query Match 3.1%; Score 19; DB 25; Length 948;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 261 AGCTATTATTATGATGCCA 279

DB 678 AGCTATTATTATGATGCCA 696

RESULT 13

AAA98873/C

ID AAA98873 standard; cDNA, 989 BP.

AC AAA98873;

DT 16-FEB-2001 (first entry)

DE Human proliferation-associated endothelial EST cDNA SEQ ID NO 18.

XX EST; expressed sequence tag; human; cell differentiation; antidiabetic;
 KW cell proliferation; endothelial tissue; angiogenic; antiposoriatic;
 KW ophthalmological; nephrotropic; cyostatic; hepatotropic; antiarthritic;
 KW antiarteriosclerotic; antirheumatic; gene therapy; angiogenic disease;
 KW treatment; rheumatoid arthritis; haemangioma; angiodioma; eye disease;
 KW diabetic retinopathy; glaucoma; kidney disease; glomerulonephritis;
 KW diabetic nephropathy; malign nephrosclerosis; transplant rejection;
 KW thrombotic microangiopathic syndrome; glomerulopathy; fibrotic disease;
 KW mesangial cell proliferative disease; ss.

OS Homo sapiens.

PN DE19911684-A1.

PD 14-SEP-2000.

PF 09-MAR-1999; 99DE-1011684.

PR 09-MAR-1999; 99DE-1011684.

PA (SCHD) SCHERING AG.

PI Glienke J, Thierauch K, Hinzmann B, Pilarsky C;

PT

DR WPI; 2000-588417/56.

XX Human nucleic acid sequences from endothelial cells useful for
 PT treatment of angiogenic disease, including psoriasis, arthritis and
 PT diabetic retinopathy, etc -

XX Claim 1a; Page 75-76; 84pp; German.

XX This invention describes novel human nucleic acid sequences (I) from
 CC endothelial cells which have angiogenic, antiposoriatic, antidiabetic,
 CC ophthalmological, nephrotropic, cyostatic, hepatotropic,
 CC antiarteriosclerotic, antiarthritic, antirheumatic activity and can be
 CC used for gene therapy. The nucleic acid sequences may find use as tools
 CC to identify agents against angiogenic diseases. The polypeptides may be
 CC used in medicaments for gene therapy to treat angiogenic diseases. (I)
 CC in sense or antisense form may be used. The genomic genes may also be
 CC used with suitable promoters and/or enhancers. The sequences (nucleic
 CC acid and proteins) may be used to treat psoriasis, arthritis, especially
 CC rheumatoid arthritis, haemangioma, angiodioma, eye diseases, especially
 CC diabetic retinopathy, neovascular glaucoma, kidney disease, such as
 CC glomerulonephritis, diabetic nephropathy, malign nephrosclerosis,
 CC thrombotic microangiopathic syndrome, transplantation rejection and
 CC glomerulopathy, fibrotic disease, such as liver cirrhosis, mesangial cell
 CC proliferative disease, arteriosclerosis and injury to nerve tissue.

XX SQ Sequence 989 BP; 261 A; 246 C; 183 G; 299 T; 0 other;

Query Match 3.1%; Score 19; DB 21; Length 989;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 282 ATTACTTTTATGCTGTT 300

DB 771 ATTACTTTTATGCTGTT 753

RESULT 14

AAA98155/C

ID AAA98155 standard; cDNA, 989 BP.

AC AAA98155;

DT 26-JAN-2001 (first entry)

DE Human proliferation-associated protein EST encoded cDNA #17.

XX Proliferation-associated protein; differentiation-associated protein;
 KW EST; expressed sequence tag; endothelial cell; anti-angiogenic;
 KW angiogenic; antiposoriatic; anti-arthritic; antifibrotic; hepatotropic;
 KW antiarteriosclerotic; nephrotropic; antidiabetic; ophthalmological;
 KW immunosuppressive; neuroprotective; gene therapy; psoriasis; arthritis;
 KW hemangioma; diabetic retinopathy; glomerulonephritis; liver cirrhosis;
 KW transplant rejection; arteriosclerosis; nervous tissue injury; human; ss.

OS Homo sapiens.

PN WO200053734-A2.

PD 14-SEP-2000.

PF 08-MAR-2000; 2000WO-EP02005.

PR 09-MAR-1999; 99DE-1011684.

PR 01-OCT-1999; 99DE-1048679.

PA (SCHD) SCHERING AG.

PI Thierauch K, Glienke J, Hinzmann B, Pilarsky C;

PT WPI; 2000-572267/53.

PT Nucleic acid sequences from human endothelial cells, useful for gene
 PT therapy of angiogenesis and for identifying antiangiogenic agents -

CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.

SO Sequence 1061 BP; 355 A; 170 C; 202 G; 319 T; 15 other;

Query Match 3.1%; Score 19; DB 22; Length 1061;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 TAAATTAATATATATAA 390
|||||
Db 802 TAAATTAATATATATAA 784

RESULT 17
AAN71064

ID AAN71064 standard; DNA; 1908 BP.

XX AAN71064;

DT 25-MAR-2003 (updated)
DT 01-JAN-1980 (first entry)

DE Gene encoding Plasmodium vivax sporozoite circumsporozoite protein.

KW Immunogen; vaccine; malaria; immunodominant epitope; ss.

XX Plasmodium vivax.

OS Plasmodium vivax.

Key Location/Qualifiers
FH 157..1293
FT CDS /tag= a
FT /product= circumsporozoite protein

PN MO8700533-A.

XX 29-JAN-1987.

PF 24-JUN-1986; 86WO-US01373.

PR 12-JUL-1985; 85US-0754645.

PR 30-MAR-1987; 87US-0032327.

PA (UNIV) UNIV NEW YORK STATE.

XX (ARNO/) ARNOT D E.

PI Arnot DE, Enea V, Nussenzwei RS, Nussenzweig V;

XX WPI; 1987-037250/05.

DR P-PSDB; AAP0708.

XX New Plasmodium vivax circumsporozoite protein - and synthetic

PT peptide(s) contg. its dominant epitope, useful in anti-malarial

XX vaccines

PS Disclosure; fig. 3; 32pp; English.

XX The circumsporozoite protein of P. vivax sporozoites encoded by

CC this gene is useful in the construction of an anti-malarial

CC vaccine. The sequence consists of a central domain of AAP70704

CC repeated 19 times plus N- and C-terminal regions (practically

CC homologous with the corresponding domains of P. cynomolgi and P.

CC knowlesi. See also AAP70704-07, AAP70709 and AAN71065.

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 1908 BP; 677 A; 353 C; 470 G; 408 T; 0 other;

Query Match 3.1%; Score 19; DB 8; Length 1908;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 TAAATTAATGAGTAA 375
|||||
Db 251 TAAATTAATGAGTAA 269

RESULT 18

AAS30510

ID AAS30510 standard; DNA; 2422 BP.

XX AAS30510;

DT 21-NOV-2001 (first entry)

DE DNA encoding novel prostate gland antigen, Seq ID No 368.

XX Human; noctropic; neuroprotective; cytostatic; antiparkinsonian;

KW antianemic; dermatological; immunosuppressive; antiinflammatory;

KW antianthratic; antineumatic; virucide; hepatotropic; nephrotropic;

KW osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;

KW prostatic; carcinoma; adenocarcinoma; benign prostatic hypertrophy;

KW hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;

KW reproductive system disorder; autoimmune disorder; urinary system;

KW systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;

KW blood-related disorder; hyperproliferative disorder; respiratory;

KW neurological disorder; endocrine disorder; inflammatory disorder;

KW liver disorder; wound healing; food preservative; ds.

XX Homo sapiens.

OS Homo sapiens.

PN WO200155447-A1.

XX 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01330.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

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PR 16-MAR-2000; 2000US-0189874.

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 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
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 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-1) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476223/51.

Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia

Claim 1; SEQ ID No 368; 512pp; English.

The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, acute bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders (glomerulonephritis), cardiovascular disorders (arrhythmias), respiratory disorders, musculoskeletal system disorders, neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), endocrine disorders (Addison's disease), gastrointestinal disorders (inflammatory disorders), liver disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) is useful to prevent skin aging, for preventing hair loss, to maintain

Query Match 3.1%; Score 19; DB 22; Length 2422;

Best Local Similarity 100.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 282 ATACTTTTATTCGTCTGT 300

Db 1593 ATACTTTTATTCGTCTGT 1611

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ID AAS30511 standard; DNA; 2422 BP.
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AC AAS30511;
XX
DT 21-NOV-2001 (first entry)
XX
DE DNA encoding novel prostate gland antigen. Seq ID No 369.
XX
KW Human; noctropic; neuroprotective; cytosolic; antiparkinsonian;
KW antihaemic; dermatological; immunosuppressive; antiinflammatory;
KW antiahrctic; antineumatic; virocid; hepatotropic; nephrotropic;
KW osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;
KW prostatic; malacoplakia; adenocarcinoma; benign prostatic hypertrophy;
KW hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;
KW reproductive system disorder; autoimmune disorder; urinary system;
KW systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;
KW blood-related disorder; hyperproliferative disorder; respiratory;
KW neurological disorder; endocrine disorder; inflammatory disorder;
KW liver disorder; wound healing; food preservative; ds.
XX
OS Homo sapiens.
XX
PN WO200155447-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01330.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-476223/51.
XX
PT Novel isolated prostate gland related polypeptide useful for diagnosis
PT and treatment of disorders of prostate such as prostatodysconia,
PT prostaticos, prostatitis, benign prostatic hypertrophy and malacoplakia
PT
XX
PS Claim 1; SEQ ID No 369; 512bp; English.
XX
XX The invention relates to novel isolated prostate gland related nucleic
XX acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
XX prognosis, prevention, and/or treatment of diseases and/or disorders of
XX the prostate such as acute non-bacterial prostatitis, chronic non-
XX bacterial prostatitis, acute bacterial prostatitis, prostatodystonia,
XX prostaticos, granulomatous prostatitis, malacoplakia, benign prostatic
XX hypertrophy or hyperplasia, and prostate neoplastic disorders, including
XX adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
XX squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
XX diagnosing and treating reproductive system disorders (Paget's disease),
XX autoimmune disorders (systemic lupus erythematosus, rheumatoid
XX arthritis), blood-related disorders (sickle cell anaemia),
XX hyperproliferative disorders, urinary system disorders
XX (glomerulonephritis), cardiovascular disorders (arrhythmias),
XX respiratory disorders, musculoskeletal system disorders, neural activity
XX and neurological disorders (Alzheimer's disease and Parkinson's disease),
XX endocrine disorders (Addison's disease), gastrointestinal disorders
XX (inflammatory disorders), liver disorders (biliary liver cirrhosis),
XX pancreatic and gall bladder disorders, disorders of the large intestine,
XX developmental and inherited disorders, diseases at the cellular level,
XX and wound healing and epithelial cell proliferation. (I) or (II) is
XX useful to prevent skin aging, for preventing hair loss, to maintain

XX
DT 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 8977.
DE
XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN W0200155320-A2.
XX
PD 02-AUG-2001.
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PF 17-JAN-2001; 2001MO-US01339.
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XX 31-JAN-2000; 2000US-0179065.
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PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0255719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.

PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX
XX DR WPI; 2001-465570/50.
XX
XX PT Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX
XX PS Disclosure; SEQ ID NO 8977; 1297pp + Sequence listing; English.
XX
XX CC The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
XX
XX SQ Sequence 2422 BP; 744 A; 493 C; 596 G; 589 T; 0 other;

Query Match 3.1%; Score 19; DB 22; Length 2422;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
DB 1593 ATTACTTTTATGCTGTT 1611

RESULT 21
AAL06290
ID AAL06290 standard; DNA; 2422 BP.
XX
XX AC AAL06290;
XX
XX DT 21-NOV-2001 (first entry)
XX
XX DE Human reproductive system related antigen DNA SEQ ID NO: 8978.
XX
XX DE Human reproductive system related antigen; reproductive system disorder;
XX
XX KM Human, reproductive system related antigen; reproductive system disorder;
XX
XX KM cancer; gene therapy; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200155320-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01339.
XX
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 11-JUL-2000; 2000US-0217496.
XX PR 14-JUL-2000; 2000US-0218290.
XX PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518-
 PR 14-AUG-2000; 2000US-0224519-
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 PR 14-AUG-2000; 2000US-0225266.
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 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226686.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
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 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0233400.
 PR 14-SEP-2000; 2000US-0233401.
 PR 14-SEP-2000; 2000US-0233403.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
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 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239395.
 PR 13-OCT-2000; 2000US-0239397.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241807.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.

PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
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 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249224.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251866.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0255678.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 XX
 PI WPI, 2001-465570/50.
 XX
 DR Isolated nucleic acid molecule encoding a reproductive system antigen
 XX is used in preventing, treating or ameliorating a medical condition -
 PT
 XX
 PS Disclosure: SEQ ID NO 6978; 1297pp + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 CC
 XX
 SQ Sequence 2422 BP; 743 A; 494 C; 595 G; 590 T; 0 other;
 Query Match 3.1%; Score 19; DB 22; Length 2422;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY . 282 ATTACTTTTATGCTGCTT 300
 DB 1593 ATTACTTTTATGCTGCTT 1611

RESULT 22
 ABX63452
 ID ABX63452 standard; cDNA; 3318 BP.
 XX
 AC ABX63452;
 XX
 DT 26-FEB-2003 (first entry)
 XX
 DE Human cDNA #452 differentially expressed in activated vascular tissue.
 XX
 KW Human; gene; ss; vascular tissue; cytosolic; atherosclerosis;
 KW cardiact; hypotensive; antidiabetic; gynaecological; vasotrophic;
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
 KW ischaemia-reperfusion injury; stroke;
 XX
 OS Homo sapiens.
 XX
 PN US2002137081-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 08-JAN-2002; 2002US-0044090.
 XX
 PR 28-JUL-2000; 2000US-222469P.
 PR 08-JAN-2001; 2001US-260483P.
 XX
 PA (BAND/) BANDMAN O.
 XX
 PI Bandman O;
 XX
 DR MPI; 2003-110597/10.
 XX
 PT Combination for diagnosing, staging, treating, or monitoring the
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,
 PT comprises several cDNAs that are differentially expressed in activated
 PT vascular tissue -
 XX
 PS Claim 1; Page -; 18pp; English.
 XX
 CC This invention relates to a combination comprising several cDNAs that
 CC are differentially expressed in activated vascular tissue. The invention
 CC also discloses a high throughput method for detecting differentially
 CC expressed cDNAs in a sample. The cDNAs of the invention may have
 CC antiarteriosclerotic, cytosolic, cardiact, hypotensive, antidiabetic;
 CC gynaecological, vasotrophic and cerebroprotective activities and may be
 CC used in gene therapy. The cDNAs of the invention may be used in a
 CC high-throughput methods for detecting differential expression of one or
 CC more cDNAs in a sample, or screening several molecules or compounds to
 CC identify a molecule or compound that specifically binds a cDNA of the
 CC invention. A protein encoded by the cDNA may be used to screen several
 CC molecules or compounds to identify a ligand that specifically binds to
 CC the protein, or to produce or purify an antibody to the protein that can
 CC be used to detect a protein in a sample or purify a natural or
 CC recombinant protein from a sample. The nucleotides may be useful for
 CC diagnosing, staging, treating, or monitoring the progression of
 CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary
 CC artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-
 CC reperfusion injury, restenosis, or stroke. The cDNAs can also be used
 CC for large-scale genetic or gene expression analysis of several new
 CC nucleic acid molecules. Antibodies to the proteins encoded by the
 CC cDNAs are useful for diagnosing pre-pathologic disorders, and chronic
 CC or acute diseases associated with abnormalities in the expression,
 CC amount or distribution of the protein. The present sequence
 CC represents a cDNA of the invention that is differentially expressed in
 CC activated vascular tissue.
 CC Note: The sequence data for this patent did not form part of the
 CC specification, but was obtained in electronic format directly from USPTO
 CC at <http://seqdata.uspto.gov/sequence.html?docID=20020137081>.
 XX
 SQ Sequence 3318 BP; 1029 A; 566 C; 628 G; 1093 T; 2 other;

Query Match 3.1%; Score 19; DB 25; Length 3318;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 261 ACCTATTTTATGATGCCA 279
 ||||||||||||||||
 DB 1507 ACCTATTTTATGATGCCA 1525
 ||||||||||||||||
 RESULT 23
 ABL15016
 ID ABL15016 standard; cDNA; 4357 BP.
 XX
 AC ABL15016;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39530.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEXE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR MPI; 2001-656860/75.
 DR P-PSDB; ABB70913.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1; SEQ ID NO 39530; 21pp + Sequence listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_ptc_sequences.
 XX
 SQ Sequence 4357 BP; 1181 A; 981 C; 970 G; 1225 T; 0 other;
 XX
 Query Match 3.1%; Score 19; DB 23; Length 4357;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 369 GAGTAAATTATATATATA 387
 ||||||||||||||||
 DB 1486 GAGTAAATTATATATATA 1504
 ||||||||||||||||
 RESULT 24
 ABL26996
 ID ABL26996 standard; DNA; 4466 BP.

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XX ABL26996;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 32461.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI, 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 32461; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB101840-AB16175) and the encoded proteins
XX (AB57737-AB12072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 4466 BP; 1268 A; 1044 C; 951 G; 1203 T; 0 other;
XX
XX Query Match 3.1%; Score 19; DB 23; Length 4466;
XX Best Local Similarity 100.0%; Pred. No. 36;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 369 GAGTAAATTTAATATA 387
XX ||||||||||||||||
XX Db 4375 GAGTAAATTTAATATA 4393
XX
XX RESULT 25
XX ABX34516
XX ID ABX34516 standard; cDNA; 5694 BP.
XX
XX AC ABX34516;
XX
XX 13-FEB-2003 (first entry)
XX
XX Human mdct cDNA SEQ ID 77.
XX
XX MDDT; human; disease detection and treatment molecule polypeptide;
XX anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
XX haemostatic; nephrotropic; antineoplastic; hepatotropic;
XX cancer therapy; protein replacement therapy; cell proliferative disorder;
XX cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
XX anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
XX Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;

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XX psoriasis; hepatitis; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200279449-A2.
XX
XX 10-OCT-2002.
XX
XX 27-MAR-2002; 2002WO-US09944.
XX
XX 28-MAR-2001; 2001US-279619P.
XX
XX 29-MAR-2001; 2001US-280067P.
XX
XX 29-MAR-2001; 2001US-280068P.
XX
XX 16-MAY-2001; 2001US-291280P.
XX
XX 17-MAY-2001; 2001US-291829P.
XX
XX 17-MAY-2001; 2001US-291849P.
XX
XX 19-JUN-2001; 2001US-299428P.
XX
XX 20-JUN-2001; 2001US-299776P.
XX
XX 20-JUN-2001; 2001US-300001P.
XX
XX (INCY) INCYTE GENOMICS INC.
XX
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
XX
XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
XX
XX Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;
XX
XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
XX
XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
XX WPI, 2003-058431/05.
XX
XX P-PSDB; AB11526.
XX
XX New purified disease detection and treatment molecule proteins and
XX polynucleotides, useful for diagnosing, treating or preventing cancers
XX (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
XX or hepatitis -
XX
XX Claim 1; SEQ ID NO 77; 339pp + Sequence Listing; English.
XX
XX This invention describes a novel disease detection and treatment molecule
XX polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
XX osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
XX antineoplastic, antiproliferative and hepatotropic activity. The polynucleotides
XX and the polypeptides of the invention can be used for gene therapy,
XX protein replacement therapy and are useful for treating a variety of
XX diseases or conditions. These polypeptides or polynucleotides are
XX particularly useful for diagnosing, treating or preventing cell
XX proliferative disorders (e.g. cancers including adenocarcinoma,
XX leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
XX disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
XX syndromes, inflammation, osteoporosis, thrombocytopenia, psoriasis or
XX hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
XX CC AB011450-AB011845, described in the disclosure of the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 5694 BP; 1558 A; 1155 C; 1210 G; 1771 T; 0 other;
XX
XX Query Match 3.1%; Score 19; DB 25; Length 5694;
XX Best Local Similarity 100.0%; Pred. No. 36;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 261 AGCTATTTTATGATGCCA 279
XX ||||||||||||||||
XX Db 3924 AGCTATTTTATGATGCCA 3942
XX
XX RESULT 26
XX AA33335/C
XX ID AA33335 standard; DNA; 5849 BP.
XX
XX AC AA33335;
XX

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PR 14-SEP-2000; 2000US-0233401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
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 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
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 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
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 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251930.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256713.
 PR 06-DEC-2000; 2000US-0251479.

PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251888.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-476223/51.
 DR
 XX
 XX Novel isolated prostate gland related polypeptide useful for diagnosis
 PT and treatment of disorders of prostate such as prostatodystonia,
 PT prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia
 PT
 XX
 PS Claim 1; SEQ ID No 367; 512bp; English.
 XX
 CC The invention relates to novel isolated prostate gland related nucleic
 CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,
 CC prognosis, prevention, and/or treatment of diseases and/or disorders of
 CC the prostate such as acute non-bacterial prostatitis, chronic non-
 CC bacterial prostatitis, acute bacterial prostatitis, prostatodystonia,
 CC prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic
 CC hypertrophy or hyperplasia, and prostate neoplastic disorders, including
 CC adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
 CC squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
 CC diagnosing and treating reproductive system disorders (Paget's disease),
 CC autoimmune disorders (systemic lupus erythematosus, rheumatoid
 CC arthritis), blood-related disorders (sickle cell anaemia),
 CC hyperproliferative disorders, urinary system disorders
 CC (glomerulonephritis), cardiovascular disorders (arrhythmias),
 CC respiratory disorders, musculoskeletal system disorders, neural activity
 CC and neurological disorders (Alzheimer's disease and Parkinson's disease),
 CC endocrine disorders (Addison's disease), gastrointestinal disorders
 CC (inflammatory disorders), liver disorders (biliary liver cirrhosis),
 CC pancreatic and gall bladder disorders, disorders of the large intestine,
 CC developmental and inherited disorders, diseases at the cellular level,
 CC and wound healing and epithelial cell proliferation. (I) or (II) is
 CC useful to prevent skin aging, for preventing hair loss, to maintain

Query March 3, 14; Score 19; DB 22; Length 10468;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 282 ATTACTTTTATGCTGTT 300
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 Db 7435 ATTACTTTTATGCTGTT 7453

RESULT 28
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 AC AAS30512;
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 DT 21-NOV-2001 (first entry)
 XX
 DE DNA encoding novel prostate gland antigen, Seq ID No 370.
 XX
 KW Human; noctropic; neuroprotective; cytosolic; antiparkinsonian;
 KW antiandemic; dermatological; immunosuppressive; antiinflammatory;
 KW antidiabetic; antirheumatic; vitruicide; hepatotropic; nephrotropic;
 KW osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;
 KW prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy;
 KW hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;
 KW reproductive system disorder; autoimmune disorder; urinary system;
 KW systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;
 KW blood-related disorder; hyperproliferative disorder; respiratory;
 KW neurological disorder; endocrine disorder; inflammatory disorder;

KW liver disorder; wound healing; food preservative; ds.
XX
OS Homo sapiens.
XX
PN MO200155447-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01330.
XX
PR 31-JUN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
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PR 11-JUL-2000; 2000US-0217487.
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PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251858.
PR 08-DEC-2000; 2000US-0251859.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI, 2001-476223/51.
XX
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PT prostatic hyperplasia, prostatic hyperplasia, benign prostatic hyperplasia and malacoplakia
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PS Claim 1, SEQ ID No 370; 512bp; English.
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CC bacterial prostatitis, acute bacterial prostatitis, prostatic hyperplasia,
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CC hyperplasia or hyperplasia, and prostate neoplastic disorders, including
CC adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and
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CC arthritis), blood-related disorders (sickle cell anaemia),
CC hyperproliferative disorders, urinary system disorders
CC (glomerulonephritis), cardiovascular disorders (arrhythmias),
CC respiratory disorders, musculoskeletal system disorders, neural activity
CC and neurological disorders (Alzheimer's disease and Parkinson's disease),
CC endocrine disorders (Addison's disease), gastrointestinal disorders
CC (inflammatory disorders), liver disorders (biliary liver cirrhosis),
CC pancreatic and gall bladder disorders, disorders of the large intestine,
CC developmental and inherited disorders, diseases at the cellular level,
CC and wound healing and epithelial cell proliferation. (I) or (II) is
CC useful to prevent skin aging, for preventing hair loss, to maintain

Query Match 3.1%; Score 19; DB 22; Length 10468;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
Db 7435 ATTACTTTTATGCTGTT 7453
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RESULT 29
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XX AAL06288;
AC
XX
XX 21-NOV-2001 (first entry)
DT
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 8976.
DE
XX
XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; de.
XX
XX Homo sapiens.
OS
XX
XX WO200155320-A2.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01339.
PF
XX
XX 31-JAN-2000; 2000US-0179065.
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XX 04-FEB-2000; 2000US-0180628.
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XX 16-MAR-2000; 2000US-0189874.
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XX 17-MAR-2000; 2000US-0190076.

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PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM,
XX
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX
XX
XX Disclosure; SEQ ID NO 8976; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
CC

CC protein of the invention.
XX
SQ Sequence 10468 BP; 2791 A; 2285 C; 2566 G; 2826 T; 0 other;
XX
Query Match 3.1%; Score 19; DB 22; Length 10468;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 282 ATTACTTTTATTGCTGTT 300
DB 7435 ATTACTTTTATTGCTGTT 7453
RESULT 30
ID AAL06291 standard; DNA; 10468 BP.
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XX AAL06291;
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XX
DT 21-NOV-2001 (first entry)
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DE Human reproductive system related antigen DNA SEQ ID NO: 8979.
XX
XX Human; reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX WO200155320-A2.
XX
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 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.

PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249266.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 06-DEC-2000; 2000US-0251856.
 PR 06-DEC-2000; 2000US-0251858.
 PR 06-DEC-2000; 2000US-0251869.
 PR 06-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-465570/50.
 DR
 XX
 XX
 PT Isolated nucleic acid molecule encoding a reproductive system antigen
 PT is used in preventing, treating or ameliorating a medical condition -
 XX
 XX
 PS Disclosure; SEQ ID NO 8979; 1297bp + Sequence Listing; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 CC
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 SQ Sequence 10468 BP; 2791 A; 2285 C; 2566 G; 2826 T; 0 other;
 Query Match 3.1%; Score 19; DB 22; Length 10468;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 282 ATTACTTTTATGCTGTT 300
 Db 7435 ATTACTTTTATGCTGTT 7453
 RESULT 31
 ABO66997
 ID ABO66997 standard; DNA; 37515 BP.
 XX
 AC ABO66997;
 XX
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Human angiogenesis associated polynucleotide SEQ ID NO 27.
 KW Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
 KW inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerd;
 KW macular degeneration; inflammatory bowel disease; Crohn's disease;
 KW antithrombotic; antiarthritic; antidiabetic; antipsoriatic;
 XX antiarteriosclerotic; ds.
 OS Homo sapiens.
 XX
 XX
 PN WO200246454-A2.
 XX

```

PD 13-JUN-2002.
XX
XX 06-DEC-2001; 2001WO-EP14320.
XX
XX 06-DEC-2000; 2000DE-1061338.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Schacht O;
XX
XX WPI; 2002-500450/53.
XX
XX New nucleic acid fragments from chemically treated
XX angiogenesis-associated genes, useful for determining methylation
XX status, e.g. in diagnosis or treatment of cancer
XX
XX Claim 1; SEQ ID NO 27; 41pp + Sequence Listing; German.
XX
XX The invention relates to a nucleic acid (I) comprising a segment of 18
XX bases of chemically pretreated DNA of angiogenesis-associated genes (II)
XX having sequences (AB066971-AB067178) or their complements, (I)' also
XX related oligomers, are used to evaluate the methylation status and/or
XX single-nucleotide polymorphisms, in angiogenesis-related genes, for
XX diagnosis and treatment of eye diseases, proliferative retinopathy,
XX neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis,
XX diabetic retinopathy, macular degeneration caused by neovascularisation,
XX psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
XX Crohn's disease.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 37515 BP; 11137 A; 425 C; 7785 G; 18168 T; 0 other;
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Query Match 3.1%; Score 19; DB 24; Length 37515;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 453 AGTATGTTATAGGTAAT 471
Db 14611 AGTATGTTATAGGTAAT 14629
RESULT 32
AB099650/c
ID AB099650 standard; DNA; 51959 BP.
XX
XX AB099650;
XX
XX 12-NOV-2002 (first entry)
XX
XX Human membrane spanning 4-domain family, subfamily A genomic sequence.
DE
XX Human, membrane spanning 4-domain A; cytosolic; antiallergic; MS4A;
KW gene therapy; atopic disorder; non-Hodgkin's lymphoma;
KW Hodgkin's lymphoma; allergic disease; gene; ss; chromosome 11q12-13.1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 29933..43739
XX /tag= a
XX /product= "MS4A"
XX /note= "Contains 5 introns"
XX /tag= b
XX /tag= c
XX /number= 1
XX /cons_splice= (5'site:NO,3'site:YES)
XX intron 30029..34942
XX /tag= c
XX /number= 1
XX exon 34943..35011
XX /tag= d
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FT 38832..40332
FT /tag= g
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FT /number= 5
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FT 43668..43736
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FT /number= 6
XX
XX WO200262946-A2.
XX
XX 15-AUG-2002.
XX
XX 10-DEC-2001; 2001WO-US48437.
XX
XX 08-DEC-2000; 2000US-254362P.
XX 20-FEB-2001; 2001US-270057P.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Tedder TF, Liang YH;
XX
XX WPI; 2002-657530/70.
XX
XX New membrane spanning 4-domain A (MS4A) genes and polypeptides, useful
XX for generating animal models of atopic disorders, for drug screening,
XX or for treating (non-) Hodgkin's lymphoma, or allergic or atopic
XX disorders in e.g. humans
XX
XX Claim 18; Page 227-255; 450pp; English.
XX
XX The invention relates to novel membrane spanning 4-domain A (MS4A)
XX nucleic acid and polypeptide molecules, comprising human and mouse
XX The polypeptides of the invention have cytosolic and antiallergic
XX activity. The polynucleotides may have a use in gene therapy. The MS4A
XX nucleic acids and polypeptides are useful for generating animal (e.g.
XX mouse) models of atopic disorders, or for drug discovery screens. These
XX are also useful for treating (non-)Hodgkin's lymphoma, allergic
XX diseases, atopic disorders or other MS4A-related conditions. The present
XX sequence represents a human MS4A genomic region.
XX
XX Sequence 51959 BP; 15233 A; 9505 C; 9853 G; 17080 T; 288 other;
SQ
Query Match 3.1%; Score 19; DB 24; Length 51959;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 349 AAGGTTTAAATTTAAAT 367
Db 35860 AAGGTTTAAATTTAAAT 35842
RESULT 33

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```

AAH68529
ID AAH68529 standard; DNA; 34980 BP.
XX
AC AAH68529;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7064.
XX
KM Corynebacterium; amino acid synthesis; vitamin; saccharide;
XX
OS organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
XX
PS Disclosure; SEQ ID NO: 7064; 246bp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of Corynebacterium bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
CC from Corynebacterium bacterium. Corynebacterium bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 349980 BP; 82466 A; 95954 C; 90516 G; 81044 T; 0 other;
XX
Query Match 3.1%; Score 19; DB 22; Length 349980;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 376 TTTAATATATATAAAGGCT 394
Db 335974 TTTAATATATATAAAGGCT 335992
XX
RESULT 34
AAH68530
ID AAH68530 standard; DNA; 34980 BP.
XX
AC AAH68530;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7065.
XX

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KM Corynebacterium bacterium; amino acid synthesis; vitamin; saccharide;
XX
OS organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
DR WPI; 2001-376931/40.
XX
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT
XX
PS Disclosure; SEQ ID NO: 7065; 246bp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of Corynebacterium bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Corynebacterium bacterium, and identifying a homologue of a gene derived
CC from Corynebacterium bacterium. Corynebacterium bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a nucleic acid described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 349980 BP; 86896 A; 98023 C; 80939 G; 84122 T; 0 other;
XX
Query Match 3.1%; Score 19; DB 22; Length 349980;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 376 TTTAATATATATAAAGGCT 394
Db 335974 TTTAATATATATAAAGGCT 35992
XX
RESULT 35
AA161373
ID AA161373 standard; DNA; 513445 BP.
XX
AC AA161373;
XX
DT 16-OCT-2001 (first entry)
XX
DE Soybean 318013 region A3, SEQ ID NO: 4.
XX
KM Soybean; antihelminthic; gene therapy; soybean cyet nematode; SCN;
KM SCN resistance; Rhg1; Rhg4; SCN resistant allele; plant breeding;
KM 240017 region G3; 318013 region A3; 515002 region G2; ds.
XX
OS Glycine max.
XX
PN WO200151627-A2.
XX
PD 19-JUN-2001.
XX

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FT      /*tag= bj
FT      /number= 4a

Query Match 3.1%; Score 19; DB 24; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 ATATGCTTTATTTATTTAT 246
Db 963911 ATATGCTTTATTTATTTAT 963893

RESULT 37
ABT01503/C
ID ABT01503 standard; DNA; 1503841 BP.
XX AC ABT01503;
XX 07-NOV-2002 (first entry)
DE Human neuregulin 1 gene.
XX DE
XX Human neuregulin 1; neuregulin-1-associated gene 1; NRGL; NRGL1;
XX Human; neuregulin 1; neuregulin-1-associated gene 1; NRGL; NRGL1;
KW schizophrenia; chromosome 8p12; single nucleotide polymorphism; SNP;
XX neuroleptic; gene therapy; gene; ds.
XX OS
XX Homo sapiens.
XX Location/Qualifiers
FH Key 244312..1369465
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FT /note= "this sequence contains introns"
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FT intron 244349..244640
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FT exon 244641..245646
FT /*tag= d
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FT intron 245647..826009
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FT intron 826102..826307
FT /*tag= g
FT /number= 3
FT exon 826308..826355

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Query Match      3.1%; Score 19; DB 24; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      228 ATATGCTTATTATTAT 246
Db      963911 ATATGCTTATTATTAT 963893

RESULT 38
AAK95240/c
ID      AAK95240 standard; DNA; 1503900 BP.
XX
AC      AAK95240;
XX
DT      17-DEC-2001 (first entry)
XX
DE      Human. neurogulin-1 gene.
XX
KW      Human; neurogulin-1 associated gene 1; NRG1AG1; Schizophrenia gene;
KM      gene therapy; ds.
XX
OS      Homo sapiens.
XX
PN      WC200164876-A2.
XX
PD      07-SEP-2001.
XX
PE      28-FEB-2001; 2001WO-US06376.
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PR      28-FEB-2000; 2000US-0515715.
XX
PA      (DECO-) DECODE GENETICS EHF.
XX
PI      Stefansson H, Steinhorsdottir V, Gulcher JR;
XX
XX      WPI; 2001-550179/61.
XX      P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905,
XX      DR      AAG67906, AAG67907, AAG67908, AAG67909, AAG67910, AAG67911, AAG67912,
XX      DR      AAG67913, AAG67914, AAG67915, AAG67916, AAG67917, AAG67918, AAG67919,
XX      DR      AAG67920, AAG67921, AAG67922, AAG67923, AAG67924, AAG67925, AAG67926,
XX      DR      AAG67927, AAG67928, AAG67929, AAG67930, AAG67931, AAG67932, AAG67933,
XX      DR      AAG67934, AAG67935, AAG67936, AAG67937.
XX
PT      Neurogulin-1 associated gene 1 nucleic acids and fragments, useful for
PT      preventing diagnosing and treating schizophrenia -
XX
XX      Disclosure; Page 90-501; 750pp; English.
XX
XX      This sequence represents the human neurogulin-1 associated gene 1
XX      (NRG1AG1) of the invention. The NRG1AG1 gene is also referred to as the
XX      human Schizophrenia gene. The invention also relates to fragments or
XX      variants of the gene and the NRG1AG1 polypeptides they encode. The
XX      NRG1AG1 nucleic acids and polypeptides may be used in the prevention,
XX      diagnosis and treatment of diseases associated with inappropriate NRG1AG1
XX      expression. For example, they may be used to treat disorders associated

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CC      with decreased expression by rectifying mutations or deletions in a
CC      patient's genome that affect the activity of NRG1AG1 by expressing
CC      inactive proteins or to supplement the patients own production of
CC      NRG1AG1. Additionally, the gene may be used to produce NRG1AG1
CC      polypeptides, by inserting the nucleic acids into a host cell and
CC      culturing the cell to express the protein. The gene may also be used as
CC      DNA probes and primers in diagnostic assays to detect and quantitate the
CC      presence of similar nucleic acids in samples, and therefore which
CC      patients may be in need of restorative therapy. The NRG1AG1 polypeptides
CC      may also be used as antigens in the production of antibodies against
CC      NRG1AG1 and in assays to identify modulators of NRG1AG1 expression and
CC      activity. Anti-NRG1AG1 antibodies and antagonists may also be used to
CC      down regulate expression and activity. Anti-NRG1AG1 antibodies may
CC      also be used as diagnostic agents for detecting the presence of NRG1AG1
CC      polypeptides in samples. NRG1AG1 is associated with schizophrenia which
CC      may be prevented, diagnosed and/or treated by the above methods.
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SQ      Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;

Query Match      3.1%; Score 19; DB 22; Length 1503900;
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Oy      228 ATATGCTTATTATTAT 246
Db      963970 ATATGCTTATTATTAT 963952

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OS      Homo sapiens.
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PD      07-SEP-2001.
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PE      28-FEB-2001; 2001WO-US06377.
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PI      Stefansson H, Steinhorsdottir V, Gulcher JR;
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XX      DR      AAG67974, AAG67975.
XX
PT      Neurogulin 1 nucleic acids and proteins useful for diagnosing
PT      preventing and treating schizophrenia -
XX
XX      Disclosure; Page 345-756; 756pp; English.
XX
XX      This sequence represents the human neurogulin 1 gene of the invention.
XX      The invention also relates to fragments or variants of the neurogulin 1
XX      gene. The gene and its proteins may be used in the prevention, diagnosis
XX      and treatment of diseases associated with inappropriate neurogulin 1
XX      expression, such as schizophrenia. For example they may be used to treat

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disorders associated with decreased neuregulin 1 expression by rectifying mutations or deletions in a patient's genome that affect the activity of neuregulin 1 by expressing inactive proteins or to supplement the patients own production of polypeptides. Additionally, the gene may be used to produce the neuregulin 1 protein, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The gene and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The protein may also be used as antigens in the production of antibodies against neuregulin 1 and in assays to identify modulators of neuregulin 1 expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of neuregulin 1 in samples.

Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;

Query Match 3.1%; Score 19; DB 22; Length 1503900;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 963970 ATATGCTTATTATTAT 963952

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KV gene; ds; single nucleotide polymorphism; SNP.
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Job time : 257 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 06:23:16 ; Search time 57 Seconds
(without alignments)
4816.497 Million cell updates/sec

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Perfect score: 622
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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C 125	15	2.4	623	1	US-08-784-289-2	Sequence 2, Appl1	198	15	2.4	2157	4	US-09-328-352-968	Sequence 968, App
C 126	15	2.4	676	4	US-08-747-562-10	Sequence 10, Appl1	199	15	2.4	2168	3	US-08-749-592-6	Sequence 6, Appl1
C 127	15	2.4	677	1	US-08-211-942-8	Sequence 6, Appl1	200	15	2.4	2210	1	US-07-710-361-2	Sequence 2, Appl1
C 128	15	2.4	732	1	US-08-211-942-6	Sequence 2295, Ap	201	15	2.4	2217	4	US-09-107-532A-1442	Sequence 1442, Ap
C 129	15	2.4	747	4	US-09-328-352-2295	Sequence 2295, Ap	202	15	2.4	2220	2	US-09-134-001C-749	Sequence 749, App
C 130	15	2.4	765	2	US-08-667-939A-12	Sequence 13, Appl1	203	15	2.4	2249	2	US-08-463-081B-34	Sequence 34, Appl1
C 131	15	2.4	765	2	US-08-667-939A-13	Sequence 13, Appl1	204	15	2.4	2249	2	US-08-463-379A-34	Sequence 34, Appl1
C 132	15	2.4	765	2	US-08-667-939A-14	Sequence 15, Appl1	205	15	2.4	2249	2	US-08-463-379A-34	Sequence 34, Appl1
C 133	15	2.4	765	2	US-08-667-939A-15	Sequence 15, Appl1	206	15	2.4	2249	3	US-08-463-074B-34	Sequence 34, Appl1
C 134	15	2.4	765	2	US-08-667-939A-16	Sequence 12, Appl1	207	15	2.4	2249	3	US-08-465-585C-34	Sequence 34, Appl1
C 135	15	2.4	765	4	US-08-433-123-12	Sequence 12, Appl1	208	15	2.4	2249	3	US-08-652-446-34	Sequence 34, Appl1
C 136	15	2.4	765	4	US-08-433-123-13	Sequence 13, Appl1	209	15	2.4	2249	3	US-08-802-117-5	Sequence 5, Appl1
C 137	15	2.4	765	4	US-08-433-123-14	Sequence 14, Appl1	210	15	2.4	2288	3	US-09-135-232-1	Sequence 11, Appl1
C 138	15	2.4	765	4	US-08-433-123-15	Sequence 15, Appl1	211	15	2.4	2288	4	US-09-026-001A-11	Sequence 1, Appl1
C 139	15	2.4	803	4	US-09-634-238-70	Sequence 70, Appl1	212	15	2.4	2288	4	US-09-863-549-1	Sequence 1, Appl1
C 140	15	2.4	831	4	US-09-328-475C-453	Sequence 253, App	213	15	2.4	2327	2	US-08-835-170-3	Sequence 3, Appl1
C 141	15	2.4	870	4	US-09-328-352-1901	Sequence 1901, Ap	214	15	2.4	2327	3	US-09-359-257-3	Sequence 3, Appl1
C 142	15	2.4	891	4	US-09-314-701-55	Sequence 55, Appl1	215	15	2.4	2334	4	US-09-371-674-3	Sequence 3, Appl1
C 143	15	2.4	933	4	US-09-328-352-3786	Sequence 3786, Ap	216	15	2.4	2347	5	US-08-062-632-4	Sequence 4, Appl1
C 144	15	2.4	942	4	US-09-107-533A-1271	Sequence 1271, Ap	217	15	2.4	2350	4	PCT-US96-03965-1	Sequence 1, Appl1
C 145	15	2.4	957	4	US-09-382-906A-1	Sequence 2278, Ap	218	15	2.4	2350	4	US-08-012-269A-1	Sequence 1, Appl1
C 146	15	2.4	960	4	US-09-328-352-2278	Sequence 2278, Ap	219	15	2.4	2383	3	US-09-523-467-9	Sequence 9, Appl1
C 147	15	2.4	1001	4	US-09-671-317-23	Sequence 23, Appl1	220	15	2.4	2400	1	US-08-785-052-3	Sequence 3, Appl1
C 148	15	2.4	1001	4	US-09-671-317-176	Sequence 176, App	221	15	2.4	2409	2	US-08-913-581-3	Sequence 9, Appl1
C 149	15	2.4	1001	4	US-09-671-317-176	Sequence 285, App	222	15	2.4	2409	3	US-09-340-095-9	Sequence 9, Appl1
C 150	15	2.4	1026	4	US-09-328-352-3052	Sequence 3052, Ap	223	15	2.4	2451	4	US-09-328-352-2551	Sequence 2551, Ap
C 151	15	2.4	1047	4	US-09-107-533A-2496	Sequence 2496, Ap	224	15	2.4	2562	4	US-09-328-352-70	Sequence 70, Appl1
C 152	15	2.4	1110	4	US-09-328-352-171	Sequence 171, App	225	15	2.4	2576	4	US-09-620-312D-1034	Sequence 1034, Ap
C 153	15	2.4	1131	4	US-09-620-312D-203	Sequence 203, App	226	15	2.4	2663	4	US-09-068-740A-8	Sequence 8, Appl1
C 154	15	2.4	1169	3	US-08-903-325-4	Sequence 4, Appl1	227	15	2.4	2685	3	US-09-061-768A-1	Sequence 1, Appl1
C 155	15	2.4	1182	4	US-09-107-533A-743	Sequence 743, App	228	15	2.4	2775	1	US-08-481-130-25	Sequence 25, Appl1
C 156	15	2.4	1251	3	US-09-330-611-1	Sequence 1, Appl1	229	15	2.4	2775	1	US-08-656-984A-25	Sequence 25, Appl1
C 157	15	2.4	1251	3	US-08-591-629-1	Sequence 16, Appl1	230	15	2.4	2775	1	US-08-485-604-25	Sequence 25, Appl1
C 158	15	2.4	1282	1	US-08-211-942-16	Sequence 39, Appl1	231	15	2.4	2910	1	US-08-487-595-25	Sequence 25, Appl1
C 159	15	2.4	1299	4	US-09-222-938A-39	Sequence 39, Appl1	232	15	2.4	2910	1	US-08-375-709-6	Sequence 6, Appl1
C 160	15	2.4	1339	3	US-08-855-910-5	Sequence 44, Appl1	233	15	2.4	2910	1	US-08-752-929-6	Sequence 6, Appl1
C 161	15	2.4	1431	1	US-07-710-361-3	Sequence 2, Appl1	234	15	2.4	2927	2	US-09-231-899-81	Sequence 81, Appl1
C 162	15	2.4	1431	3	US-09-316-083-2	Sequence 12, Appl1	235	15	2.4	2927	1	US-08-737-752A-27	Sequence 27, Appl1
C 163	15	2.4	1487	3	US-07-865-662F-11	Sequence 11, Appl1	236	15	2.4	2927	1	US-08-481-130-27	Sequence 27, Appl1
C 164	15	2.4	1487	3	US-08-374-219B-11	Sequence 11, Appl1	237	15	2.4	2927	1	US-08-666-984A-27	Sequence 27, Appl1
C 165	15	2.4	1503	4	US-09-328-352-4057	Sequence 4057, Ap	238	15	2.4	2927	1	US-08-485-604-27	Sequence 27, Appl1
C 166	15	2.4	1551	4	US-09-625-972-19	Sequence 19, Appl1	239	15	2.4	2927	2	US-08-487-595-27	Sequence 27, Appl1
C 167	15	2.4	1620	2	US-08-874-186-37	Sequence 37, Appl1	240	15	2.4	2999	2	US-09-014-969-8	Sequence 8, Appl1
C 168	15	2.4	1642	4	US-09-737-698B-24	Sequence 24, Appl1	241	15	2.4	3003	1	US-08-434-730-15	Sequence 15, Appl1
C 169	15	2.4					242	15	2.4	3054	4	US-09-134-001C-705	Sequence 705, App
C 170	15	2.4					243	15	2.4	3073	1	US-07-668-352C-31	Sequence 31, Appl1
C 171	15	2.4					244	15	2.4	3073	2	US-08-474-379C-31	Sequence 31, Appl1
C 172	15	2.4					245	15	2.4	3073	3	US-09-146-249A-31	Sequence 31, Appl1
C 173	15	2.4					246	15	2.4	3073	3	US-08-206-188B-31	Sequence 31, Appl1

247	15	2.4	3073	5	PCT-US91-02714-30	Sequence 30, Appl	320	15	2.4	7560	3	US-09-103-478-4	Sequence 4, Appl
248	15	2.4	3266	4	US-08-485-511A-3	Sequence 3, Appl	321	15	2.4	7560	4	US-09-193-931C-4	Sequence 4, Appl
249	15	2.4	3412	3	US-08-903-325-3	Sequence 3, Appl	322	15	2.4	7560	4	US-09-026-221-4	Sequence 4, Appl
250	15	2.4	3505	1	US-07-660-465-1	Sequence 1, Appl	323	15	2.4	8378	5	PCT-US91-09055-1	Sequence 1, Appl
251	15	2.4	3632	1	US-08-424-788-4	Sequence 1, Appl	324	15	2.4	9641	4	US-09-625-972-22	Sequence 22, Appl
252	15	2.4	3632	1	US-08-110-683-1	Sequence 1, Appl	325	15	2.4	10640	4	US-09-417-4850-5	Sequence 5, Appl
253	15	2.4	3632	2	US-08-683-743-1	Sequence 1, Appl	326	15	2.4	12597	4	US-09-705-299-12	Sequence 12, Appl
254	15	2.4	3632	2	US-08-477-166-1	Sequence 1, Appl	327	15	2.4	14796	3	US-08-975-080-35	Sequence 35, Appl
255	15	2.4	3632	2	US-08-472-097-1	Sequence 1, Appl	328	15	2.4	14796	3	US-09-630-706-10	Sequence 10, Appl
256	15	2.4	3632	2	US-09-439-672-1	Sequence 1, Appl	329	15	2.4	15378	3	US-09-496-6948-3	Sequence 3, Appl
257	15	2.4	3632	4	US-09-495-052-57	Sequence 57, Appl	330	15	2.4	15378	3	US-08-785-420-1	Sequence 1, Appl
258	15	2.4	3632	5	PCT-US93-11638-1	Sequence 1, Appl	331	15	2.4	20966	4	US-08-961-527-54	Sequence 54, Appl
259	15	2.4	3735	4	US-09-620-312D-52	Sequence 52, Appl	332	15	2.4	25464	4	US-09-326-480A-4	Sequence 4, Appl
260	15	2.4	3780	4	US-09-134-001C-920	Sequence 920, App	333	15	2.4	30310	4	US-09-657-346A-96	Sequence 96, Appl
261	15	2.4	3883	4	US-09-620-312D-792	Sequence 792, App	334	15	2.4	34466	4	US-09-103-330-35	Sequence 35, Appl
262	15	2.4	3934	3	US-09-226-568-18	Sequence 18, Appl	335	15	2.4	36651	4	US-09-738-894A-3	Sequence 3, Appl
263	15	2.4	3946	1	US-08-077-848A-1	Sequence 1, Appl	336	15	2.4	36651	4	US-09-964-469-3	Sequence 3, Appl
264	15	2.4	3946	3	US-09-211-640-1	Sequence 1, Appl	337	15	2.4	37895	1	US-08-375-709-1	Sequence 1, Appl
265	15	2.4	3946	3	US-09-378-536-1	Sequence 1, Appl	338	15	2.4	37895	1	US-08-752-929-1	Sequence 1, Appl
266	15	2.4	3946	4	US-09-687-260-1	Sequence 1, Appl	339	15	2.4	37895	3	US-09-090-793-1	Sequence 1, Appl
267	15	2.4	3946	5	PCT-US94-03547-1	Sequence 1, Appl	340	15	2.4	37895	4	US-09-231-899-1	Sequence 1, Appl
268	15	2.4	3986	2	US-08-627-254C-27	Sequence 27, Appl	341	15	2.4	45175	4	US-09-453-702B-116	Sequence 116, App
269	15	2.4	4049	1	US-08-162-809-17	Sequence 17, Appl	342	15	2.4	49795	4	US-09-453-702B-60	Sequence 60, Appl
270	15	2.4	4060	1	US-08-164-292B-1	Sequence 1, Appl	343	15	2.4	62804	4	US-09-800-960-3	Sequence 3, Appl
271	15	2.4	4060	1	US-08-164-292B-3	Sequence 3, Appl	344	15	2.4	62804	4	US-09-873-404-3	Sequence 3, Appl
272	15	2.4	4060	1	US-08-164-292B-5	Sequence 5, Appl	345	15	2.4	66804	4	US-09-740-041-3	Sequence 3, Appl
273	15	2.4	4060	1	US-08-164-292B-7	Sequence 7, Appl	346	15	2.4	63588	4	US-09-811-469-3	Sequence 3, Appl
274	15	2.4	4060	3	US-08-845-623-1	Sequence 1, Appl	347	15	2.4	116592	4	US-09-818-512-3	Sequence 3, Appl
275	15	2.4	4060	3	US-08-845-623-3	Sequence 3, Appl	348	15	2.4	116592	4	US-09-661-596A-76	Sequence 76, Appl
276	15	2.4	4060	3	US-08-845-623-5	Sequence 5, Appl	349	15	2.4	14864	4	US-09-801-876B-3	Sequence 3, Appl
277	15	2.4	4060	3	US-08-845-623-7	Sequence 7, Appl	350	15	2.4	14867	4	US-09-801-876B-3	Sequence 3, Appl
278	15	2.4	4060	3	US-08-815-927-1	Sequence 1, Appl	351	15	2.4	202001	4	US-09-734-674-3	Sequence 1, Appl
279	15	2.4	4060	3	US-08-815-927-3	Sequence 3, Appl	352	15	2.4	580073	4	US-08-545-528D-1	Sequence 1, Appl
280	15	2.4	4060	3	US-08-815-927-5	Sequence 5, Appl	353	15	2.4	580073	4	US-08-545-528D-1	Sequence 1, Appl
281	15	2.4	4060	3	US-08-815-927-7	Sequence 7, Appl	354	14	2.3	20	4	US-08-837-201C-31	Sequence 31, Appl
282	15	2.4	4060	3	US-09-103-330-1	Sequence 3, Appl	355	14	2.3	20	4	US-09-364-416-31	Sequence 31, Appl
283	15	2.4	4060	4	US-09-103-330-3	Sequence 3, Appl	356	14	2.3	21	1	US-09-198-452A-6558	Sequence 6558, Ap
284	15	2.4	4060	4	US-09-103-330-5	Sequence 5, Appl	357	14	2.3	39	3	US-08-792-832A-8	Sequence 8, Appl
285	15	2.4	4060	4	US-09-103-330-7	Sequence 7, Appl	358	14	2.3	47	4	US-09-422-978-1211	Sequence 1211, Ap
286	15	2.4	4060	4	US-09-435-242-1	Sequence 1, Appl	359	14	2.3	51	4	US-09-281-495-54	Sequence 54, Appl
287	15	2.4	4060	4	US-09-435-242-3	Sequence 3, Appl	360	14	2.3	56	1	US-08-081-539-47	Sequence 47, Appl
288	15	2.4	4060	4	US-09-435-242-5	Sequence 5, Appl	361	14	2.3	56	1	US-08-466-647-47	Sequence 47, Appl
289	15	2.4	4060	4	US-09-435-242-7	Sequence 7, Appl	362	14	2.3	58	1	US-08-081-539-46	Sequence 46, Appl
290	15	2.4	4060	2	US-08-568-459A-1	Sequence 1, Appl	363	14	2.3	58	1	US-08-466-647-46	Sequence 46, Appl
291	15	2.4	4084	4	US-08-487-826B-1	Sequence 1, Appl	364	14	2.3	59	3	US-07-602-848B-11	Sequence 11, Appl
292	15	2.4	4084	4	US-09-210-288-1	Sequence 1, Appl	365	14	2.3	64	4	US-08-516-859A-95	Sequence 95, Appl
293	15	2.4	4084	6	5198347-5	Patent No. 5198347	366	14	2.3	64	4	US-09-586-472-95	Sequence 95, Appl
294	15	2.4	4097	1	US-08-162-809-11	Sequence 11, Appl	367	14	2.3	91	4	US-09-528-706-95	Sequence 95, Appl
295	15	2.4	4121	4	US-09-604-978-4	Sequence 4, Appl	368	14	2.3	91	4	US-09-313-294A-3287	Sequence 3287, Ap
296	15	2.4	4121	4	US-09-604-978-4	Sequence 4, Appl	369	14	2.3	165	3	US-08-816-346-37	Sequence 37, Appl
297	15	2.4	4334	2	US-08-670-707A-38	Sequence 38, Appl	370	14	2.3	165	3	US-09-335-411-37	Sequence 37, Appl
298	15	2.4	4334	3	US-09-037-601-38	Sequence 38, Appl	371	14	2.3	194	4	US-09-702-705-1450	Sequence 1450, Ap
299	15	2.4	4334	3	US-09-315-179-8	Sequence 38, Appl	372	14	2.3	194	4	US-09-736-457-1450	Sequence 1450, Ap
300	15	2.4	4334	3	US-09-187-049-1	Sequence 1, Appl	373	14	2.3	205	1	US-07-687-466B-3	Sequence 3, Appl
301	15	2.4	4404	4	US-09-523-656-37	Sequence 37, Appl	374	14	2.3	225	4	US-09-107-532A-1774	Sequence 1774, Ap
302	15	2.4	4832	4	US-09-457-037B-2	Sequence 2, Appl	375	14	2.3	231	4	US-09-134-001C-84	Sequence 84, Appl
303	15	2.4	4832	4	US-09-733-151-2	Sequence 2, Appl	376	14	2.3	241	4	US-09-016-434-746	Sequence 746, App
304	15	2.4	4832	4	US-08-110-158-5	Sequence 5, Appl	377	14	2.3	258	4	US-09-134-001C-1148	Sequence 1148, Ap
305	15	2.4	4946	3	US-08-817-188-1	Sequence 1, Appl	378	14	2.3	265	4	US-09-280-116-33	Sequence 33, Appl
306	15	2.4	4946	4	US-09-457-037B-1	Sequence 1, Appl	379	14	2.3	273	4	US-09-134-001C-2061	Sequence 2061, Ap
307	15	2.4	4946	4	US-09-733-151-1	Sequence 1, Appl	380	14	2.3	275	4	US-09-702-705-1243	Sequence 1243, Ap
308	15	2.4	5864	3	US-08-894-440-4	Sequence 4, Appl	381	14	2.3	275	4	US-09-736-457-1243	Sequence 1243, Ap
309	15	2.4	5864	4	US-09-458-093-4	Sequence 4, Appl	382	14	2.3	280	4	US-09-313-294A-831	Sequence 831, App
310	15	2.4	5865	4	US-09-430-487A-1	Sequence 1, Appl	383	14	2.3	292	3	US-09-037-890B-15	Sequence 15, Appl
311	15	2.4	6030	1	US-08-441-139-8	Sequence 8, Appl	384	14	2.3	294	4	US-09-134-001C-2032	Sequence 2032, Ap
312	15	2.4	6233	1	US-09-620-312D-459	Sequence 459, App	385	14	2.3	294	4	US-09-313-294A-6046	Sequence 6046, Ap
313	15	2.4	6302	4	US-09-620-312D-461	Sequence 461, App	386	14	2.3	297	4	US-09-313-294A-7286	Sequence 7286, Ap
314	15	2.4	6384	4	US-09-620-312D-460	Sequence 460, App	387	14	2.3	300	4	US-09-313-294A-6323	Sequence 6323, Ap
315	15	2.4	6402	2	US-08-670-707A-36	Sequence 36, Appl	388	14	2.3	300	4	US-09-205-258A-143	Sequence 143, App
316	15	2.4	6402	3	US-09-037-601-36	Sequence 36, Appl	389	14	2.3	307	4	US-09-313-294A-6004	Sequence 6004, Ap
317	15	2.4	6402	3	US-09-315-179-36	Sequence 36, Appl	390	14	2.3	315	1	US-08-081-539-89	Sequence 89, Appl
318	15	2.4	6402	4	US-09-523-656-29	Sequence 29, Appl	391	14	2.3	315	1	US-08-466-647-89	Sequence 89, Appl
319	15	2.4	6474	4	US-08-961-527-155	Sequence 155, App	392	14	2.3	332	3	US-08-943-731-106	Sequence 106, Appl

393	14	2.3	357	4	US-09-134-001C-802	Sequence 802, App	466	14	2.3	526	1	US-08-700-575-1	Sequence 1, Appl
C 394	14	2.3	359	3	US-08-905-223-247	Sequence 247, App	467	14	2.3	543	4	US-09-648-004-1	Sequence 1, Appl
395	14	2.3	361	3	US-08-905-223-142	Sequence 142, App	468	14	2.3	546	4	US-09-328-352-180	Sequence 180, App
396	14	2.3	369	3	US-08-991-789A-110	Sequence 190, App	C 469	14	2.3	549	4	US-09-328-352-1559	Sequence 1559, App
397	14	2.3	369	4	US-09-062-451-190	Sequence 190, App	470	14	2.3	552	4	US-09-702-705-712	Sequence 712, App
398	14	2.3	369	4	US-09-598-326-190	Sequence 190, App	471	14	2.3	552	4	US-09-736-457-712	Sequence 712, App
399	14	2.3	369	4	US-09-289-198-190	Sequence 190, App	472	14	2.3	558	3	US-09-328-111-221	Sequence 221, App
C 400	14	2.3	372	4	US-09-702-705-226	Sequence 226, App	473	14	2.3	583	3	US-09-328-111-221	Sequence 221, App
C 401	14	2.3	372	4	US-09-736-457-226	Sequence 226, App	C 474	14	2.3	590	1	US-08-463-115-15	Sequence 15, Appl
C 402	14	2.3	372	4	US-09-328-352-1906	Sequence 1906, App	C 475	14	2.3	590	1	US-08-463-115-15	Sequence 15, Appl
C 403	14	2.3	372	4	US-09-328-352-2837	Sequence 2837, App	C 476	14	2.3	592	4	US-08-585-593A-27	Sequence 27, Appl
C 404	14	2.3	375	4	US-09-328-352-3725	Sequence 3725, App	C 477	14	2.3	597	4	US-09-328-352-825	Sequence 825, App
C 405	14	2.3	380	4	US-09-288-143-53	Sequence 53, App	C 478	14	2.3	610	4	US-09-221-017B-1069	Sequence 1069, App
C 406	14	2.3	399	3	US-09-242-216-1	Sequence 1, Appl	C 479	14	2.3	613	4	US-09-149-476-15	Sequence 15, Appl
C 407	14	2.3	399	4	US-09-134-001C-1761	Sequence 1761, App	C 480	14	2.3	618	1	US-08-155-171B-5	Sequence 5, Appl
C 408	14	2.3	414	4	US-09-071-035-53	Sequence 53, App	481	14	2.3	618	2	US-08-435-998-5	Sequence 5, Appl
C 409	14	2.3	415	2	US-08-481-658B-28	Sequence 28, App	C 482	14	2.3	630	4	US-09-134-001C-1143	Sequence 1143, App
C 410	14	2.3	415	2	US-08-477-504A-28	Sequence 28, App	C 483	14	2.3	631	4	US-09-059-625-41	Sequence 41, Appl
C 411	14	2.3	415	2	US-08-486-756A-28	Sequence 28, App	C 484	14	2.3	639	4	US-09-134-001C-2133	Sequence 2133, App
C 412	14	2.3	415	2	US-08-485-862B-28	Sequence 28, App	C 485	14	2.3	642	4	US-09-107-532A-1906	Sequence 1906, App
C 413	14	2.3	415	3	US-08-487-077A-28	Sequence 28, App	C 486	14	2.3	645	4	US-09-134-001C-1986	Sequence 1986, App
C 414	14	2.3	415	3	US-08-485-863A-28	Sequence 28, App	C 487	14	2.3	648	1	US-07-872-678A-3	Sequence 3, Appl
C 415	14	2.3	415	3	US-08-485-049D-28	Sequence 28, App	C 488	14	2.3	653	3	US-08-998-416-46	Sequence 46, Appl
C 416	14	2.3	425	4	US-09-000-266-25	Sequence 25, App	C 489	14	2.3	657	3	US-09-037-990B-2	Sequence 2, Appl
C 417	14	2.3	425	4	US-09-000-266-27	Sequence 27, App	C 490	14	2.3	660	4	US-09-702-705-176	Sequence 176, App
C 418	14	2.3	425	4	US-09-628-099-25	Sequence 25, App	491	14	2.3	660	4	US-09-736-457-176	Sequence 176, App
C 419	14	2.3	425	4	US-09-628-099-27	Sequence 27, App	C 492	14	2.3	666	4	US-09-435-019-11	Sequence 11, Appl
C 420	14	2.3	425	4	US-10-056-360-25	Sequence 25, App	C 493	14	2.3	666	4	US-09-435-019-12	Sequence 12, Appl
C 421	14	2.3	425	4	US-10-056-360-27	Sequence 27, App	494	14	2.3	670	3	US-09-040-984-7	Sequence 7, Appl
C 422	14	2.3	425	4	US-10-056-359-25	Sequence 25, App	495	14	2.3	670	4	US-09-123-912-7	Sequence 7, Appl
C 423	14	2.3	433	2	US-08-967-101-34	Sequence 27, App	496	14	2.3	670	4	US-09-643-597-7	Sequence 7, Appl
C 424	14	2.3	433	2	US-08-592-541-34	Sequence 34, App	497	14	2.3	670	4	US-09-480-884A-7	Sequence 7, Appl
C 425	14	2.3	433	3	US-09-124-698-34	Sequence 34, App	498	14	2.3	670	4	US-09-542-615A-7	Sequence 7, Appl
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C 427	14	2.3	433	3	US-08-496-841C-34	Sequence 34, App	C 500	14	2.3	678	4	US-09-205-258-187	Sequence 187, App
C 428	14	2.3	433	3	US-09-124-523-34	Sequence 34, App	C 501	14	2.3	681	4	US-09-410-464-3	Sequence 3, Appl
C 429	14	2.3	433	4	US-09-636-796A-34	Sequence 34, App	C 502	14	2.3	686	1	US-08-591-498-15	Sequence 15, Appl
C 430	14	2.3	433	4	US-08-431-048P-34	Sequence 34, App	503	14	2.3	688	1	US-08-463-115-40	Sequence 44, Appl
C 431	14	2.3	435	4	US-09-007-119-3	Sequence 3, Appl	504	14	2.3	688	1	US-08-465-398-44	Sequence 44, Appl
C 432	14	2.3	445	3	US-08-787-739-28	Sequence 28, App	505	14	2.3	716	3	US-08-998-416-795	Sequence 795, App
C 433	14	2.3	445	3	US-09-178-115-28	Sequence 28, App	506	14	2.3	717	4	US-09-328-352-887	Sequence 887, App
C 434	14	2.3	445	3	US-09-177-776-28	Sequence 28, App	507	14	2.3	719	3	US-08-983-409-6	Sequence 6, Appl
C 435	14	2.3	446	3	US-09-097-541-1	Sequence 1, Appl	C 508	14	2.3	721	4	US-09-663-600A-65	Sequence 65, Appl
C 436	14	2.3	446	4	US-09-333-214-1	Sequence 1, Appl	C 509	14	2.3	726	4	US-09-134-001C-2091	Sequence 2091, App
C 437	14	2.3	447	4	US-09-134-001C-2777	Sequence 2777, App	C 510	14	2.3	729	4	US-09-059-625-43	Sequence 43, Appl
C 438	14	2.3	453	4	US-09-134-001C-2664	Sequence 2664, App	C 511	14	2.3	729	4	US-09-059-625-44	Sequence 44, Appl
C 439	14	2.3	453	4	US-09-134-001C-2664	Sequence 2664, App	C 512	14	2.3	729	4	US-09-059-625-47	Sequence 47, Appl
C 440	14	2.3	461	4	US-09-536-051C-2664	Sequence 18, App	C 513	14	2.3	735	4	US-09-107-532A-235	Sequence 235, App
C 441	14	2.3	467	3	US-09-328-111-329	Sequence 329, App	C 514	14	2.3	750	4	US-09-252-991A-10876	Sequence 10876, App
C 442	14	2.3	468	4	US-09-107-532A-1610	Sequence 1610, App	515	14	2.3	765	4	US-09-328-352-1067	Sequence 3067, App
C 443	14	2.3	475	2	US-08-623-906A-4	Sequence 4, Appl	C 516	14	2.3	783	4	US-09-134-001C-1622	Sequence 1622, App
C 444	14	2.3	483	4	US-09-306-564-4	Sequence 4, Appl	C 517	14	2.3	783	5	PCT-US92-00282-22	Sequence 22, Appl
C 445	14	2.3	486	1	US-08-048-164A-1	Sequence 1, Appl	C 518	14	2.3	798	4	US-09-463-451-25	Sequence 25, Appl
C 446	14	2.3	486	1	US-08-048-164A-3	Sequence 3, Appl	519	14	2.3	798	4	US-09-463-451-26	Sequence 26, Appl
C 447	14	2.3	486	1	US-08-048-164A-3	Sequence 3, Appl	C 520	14	2.3	799	4	US-09-166-350-11	Sequence 11, Appl
C 448	14	2.3	486	1	US-08-460-463-1	Sequence 1, Appl	C 521	14	2.3	801	4	US-09-134-001C-2084	Sequence 2084, App
C 449	14	2.3	486	1	US-08-460-463-3	Sequence 3, Appl	C 522	14	2.3	807	4	US-09-328-352-2003	Sequence 2003, App
C 450	14	2.3	486	1	US-08-460-467-1	Sequence 1, Appl	C 523	14	2.3	811	3	US-08-961-083-197	Sequence 197, App
C 451	14	2.3	486	1	US-08-460-457-3	Sequence 3, Appl	524	14	2.3	811	4	US-09-536-784-197	Sequence 197, App
C 452	14	2.3	486	1	US-08-460-458-1	Sequence 1, Appl	C 525	14	2.3	816	4	US-09-134-001C-2462	Sequence 2462, App
C 453	14	2.3	486	1	US-08-460-458-3	Sequence 3, Appl	C 526	14	2.3	825	3	US-09-250-677-1	Sequence 1, Appl
C 454	14	2.3	486	2	US-08-460-455-1	Sequence 1, Appl	C 527	14	2.3	840	4	US-09-328-352-1018	Sequence 3018, App
C 455	14	2.3	486	2	US-08-460-455-3	Sequence 3, Appl	C 528	14	2.3	849	4	US-09-107-532A-3358	Sequence 3358, App
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C 458	14	2.3	497	3	US-09-280-116-90	Sequence 90, Appl	C 531	14	2.3	866	3	US-09-122-400B-4	Sequence 4, Appl
C 459	14	2.3	499	3	US-09-284-782-21	Sequence 21, Appl	C 532	14	2.3	867	4	US-09-134-001C-1168	Sequence 1168, App
C 460	14	2.3	499	3	US-09-006-636-5	Sequence 5, Appl	533	14	2.3	870	4	US-09-328-352-1901	Sequence 1901, App
C 461	14	2.3	499	4	US-09-006-636-5	Sequence 5, Appl	534	14	2.3	888	4	US-09-134-001C-752	Sequence 752, App
C 462	14	2.3	499	4	US-09-325-274-5	Sequence 4, Appl	C 535	14	2.3	891	4	US-09-328-352-1976	Sequence 1976, App
C 463	14	2.3	504	1	US-08-460-739-4	Sequence 4, Appl	536	14	2.3	913	1	US-08-217-327-3	Sequence 3, Appl
C 464	14	2.3	508	4	US-08-858-207A-227	Sequence 227, App	537	14	2.3	913	1	US-07-885-970A-3	Sequence 3, Appl
C 465	14	2.3	516	4	US-09-601-198-79	Sequence 79, Appl	538	14	2.3	913	1	US-08-298-687A-3	Sequence 3, Appl

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541	14	2.3	913	2	US-08-787-335-2	Sequence 2, Appli	614	14	2.3	1237	4	US-09-134-001C-2376	Sequence 2376, Ap
542	14	2.3	924	4	US-09-071-035-137	Sequence 137, App	C 615	14	2.3	1242	4	US-08-705-477E-95	Sequence 95, Appl
543	14	2.3	924	4	US-09-252-991A-969	Sequence 969, App	C 617	14	2.3	1245	4	US-09-134-001C-520	Sequence 520, App
544	14	2.3	927	4	US-09-107-532A-271	Sequence 271, App	618	14	2.3	1246	3	US-09-236-080-1	Sequence 1, Appli
545	14	2.3	930	4	US-09-328-352-3511	Sequence 3511, Ap	619	14	2.3	1247	3	US-09-178-115-110	Sequence 110, App
546	14	2.3	933	4	US-09-107-532A-558	Sequence 558, App	620	14	2.3	1247	3	US-09-177-776-110	Sequence 110, App
547	14	2.3	939	1	US-08-094-138A-26	Sequence 26, Appl	621	14	2.3	1257	1	US-08-161-286-3	Sequence 3, Appli
548	14	2.3	939	1	US-08-455-674-26	Sequence 26, Appl	C 621	14	2.3	1260	1	US-08-599-252-80	Sequence 80, Appl
549	14	2.3	939	1	US-08-455-992-26	Sequence 26, Appl	C 622	14	2.3	1260	1	US-08-436-074-53	Sequence 53, Appl
550	14	2.3	939	1	US-08-455-972-26	Sequence 26, Appl	C 623	14	2.3	1262	4	US-09-101-068-3	Sequence 3, Appli
551	14	2.3	939	1	US-09-252-991A-925	Sequence 925, App	624	14	2.3	1260	5	PCT-US96-06352-80	Sequence 80, Appl
552	14	2.3	939	5	PCT-US92-00652-26	Sequence 26, Appl	625	14	2.3	1260	5	PCT-US96-06583-80	Sequence 80, Appl
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554	14	2.3	945	4	US-09-601-198-177	Sequence 177, App	C 627	14	2.3	1278	4	US-09-134-001C-58	Sequence 58, Appl
555	14	2.3	946	4	US-09-410-464-2	Sequence 2, Appli	C 628	14	2.3	1282	3	US-08-961-083-171	Sequence 171, App
556	14	2.3	948	4	US-09-134-001C-2609	Sequence 2609, Ap	629	14	2.3	1282	4	US-09-536-784-171	Sequence 171, App
557	14	2.3	949	4	US-09-221-017B-615	Sequence 615, App	C 630	14	2.3	1315	2	US-08-087-797-1	Sequence 1, Appli
558	14	2.3	960	4	US-09-107-532A-736	Sequence 736, App	631	14	2.3	1316	2	US-08-684-687-3	Sequence 3, Appli
559	14	2.3	978	4	US-09-328-352-3711	Sequence 3711, Ap	632	14	2.3	1316	4	US-08-851-520-3	Sequence 3, Appli
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564	14	2.3	1001	3	US-08-882-501-32	Sequence 32, Appl	C 637	14	2.3	1346	4	US-09-364-230-5	Sequence 5, Appli
565	14	2.3	1001	4	US-09-641-638-92	Sequence 92, Appl	C 638	14	2.3	1353	4	US-09-134-001C-1974	Sequence 1974, Ap
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567	14	2.3	1001	4	US-09-641-638-94	Sequence 94, Appl	640	14	2.3	1364	1	US-08-621-493-3	Sequence 3, Appli
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569	14	2.3	1001	4	US-09-641-638-304	Sequence 304, App	642	14	2.3	1364	3	US-09-260-173-3	Sequence 3, Appli
570	14	2.3	1001	4	US-09-641-638-367	Sequence 367, App	643	14	2.3	1368	4	US-09-227-357-98	Sequence 98, Appl
571	14	2.3	1001	4	US-09-641-638-463	Sequence 463, App	C 644	14	2.3	1373	4	US-09-996-243-7	Sequence 7, Appli
572	14	2.3	1001	4	US-09-671-317-255	Sequence 255, App	645	14	2.3	1389	4	US-09-328-352-1371	Sequence 1371, Ap
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574	14	2.3	1001	4	US-09-671-317-460	Sequence 460, App	647	14	2.3	1397	5	US-07-964-589-1	Sequence 1, Appli
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590	14	2.3	1102	5	PCT-US92-09382-1	Sequence 1, Appli	C 663	14	2.3	1513	4	US-09-686-583B-41	Sequence 41, Appl
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592	14	2.3	1110	3	US-09-252-991A-1014	Sequence 1014, Ap	665	14	2.3	1522	2	US-08-481-658B-1	Sequence 1, Appli
593	14	2.3	1116	3	US-08-918-249-3	Sequence 3, Appli	666	14	2.3	1522	2	US-08-477-504A-1	Sequence 1, Appli
594	14	2.3	1116	3	US-09-345-603-3	Sequence 3, Appli	667	14	2.3	1522	2	US-08-486-756A-1	Sequence 1, Appli
595	14	2.3	1116	4	US-09-252-991A-3059	Sequence 3059, Ap	668	14	2.3	1522	2	US-08-485-862B-1	Sequence 1, Appli
596	14	2.3	1119	3	US-08-918-249-1	Sequence 1, Appli	669	14	2.3	1522	3	US-08-787-739-1	Sequence 1, Appli
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600	14	2.3	1128	4	US-09-601-198-107	Sequence 107, App	673	14	2.3	1522	3	US-09-178-115-1	Sequence 1, Appli
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602	14	2.3	1137	6	5171843-8	Parent No. 5171843	675	14	2.3	1522	4	US-09-620-312D-96	Sequence 96, Appl
603	14	2.3	1137	6	US-09-277-716-21	Sequence 21, Appl	676	14	2.3	1524	4	US-09-134-001C-1141	Sequence 1141, Ap
604	14	2.3	1146	3	US-09-609-161B-21	Sequence 21, Appl	677	14	2.3	1530	4	US-09-328-352-739	Sequence 739, App
605	14	2.3	1152	4	US-09-134-001C-592	Sequence 592, App	678	14	2.3	1532	3	US-09-118-324-1	Sequence 1, Appli
606	14	2.3	1155	4	US-09-252-991A-7856	Sequence 7856, Ap	679	14	2.3	1566	4	US-09-134-001C-1453	Sequence 1453, Ap
607	14	2.3	1156	4	US-09-620-312D-102	Sequence 102, App	680	14	2.3	1579	4	US-09-591-095-9	Sequence 9, Appli
608	14	2.3	1156	4	US-09-134-001C-886	Sequence 886, App	681	14	2.3	1586	4	US-09-345-473E-1	Sequence 1, Appli
609	14	2.3	1189	2	US-08-450-042A-2	Sequence 2, Appli	682	14	2.3	1606	4	US-09-620-312D-99	Sequence 99, Appl
610	14	2.3	1212	2	US-08-449-933-5	Sequence 5, Appli	C 683	14	2.3	1610	2	US-08-540-804-17	Sequence 17, Appl
611	14	2.3	1212	3	US-07-966-049A-5	Sequence 5, Appli	C 684	14	2.3	1610	2	US-08-218-265-17	Sequence 17, Appl

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C 686	14	2.3	1610	3	US-08-590-399-17	Sequence 17, Appl	C 759	14	2.3	2156	4	US-09-911-888-18	Sequence 18, Appl
C 687	14	2.3	1615	2	US-08-491-988-15	Sequence 15, Appl	C 760	14	2.3	2157	2	US-08-132-990A-7	Sequence 7, Appl
C 688	14	2.3	1621	4	US-09-227-357-29	Sequence 29, Appl	C 761	14	2.3	2157	5	PCT-US92-09382-7	Sequence 7, Appl
C 689	14	2.3	1624	4	US-08-491-988-14	Sequence 14, Appl	C 762	14	2.3	2170	4	US-09-172-339-1	Sequence 21, Appl
C 690	14	2.3	1635	5	PCT-US94-05795-11	Sequence 11, Appl	C 763	14	2.3	2170	4	US-09-398-395A-21	Sequence 21, Appl
C 691	14	2.3	1637	5	US-08-063-552-3	Sequence 3, Appl	C 764	14	2.3	2170	4	US-09-887-586A-21	Sequence 21, Appl
C 692	14	2.3	1637	5	PCT-US93-05704-3	Sequence 3, Appl	C 765	14	2.3	2170	4	US-09-895-752-21	Sequence 21, Appl
C 693	14	2.3	1640	3	US-08-781-250-13	Sequence 1, Appl	C 766	14	2.3	2170	4	US-09-903-012B-21	Sequence 21, Appl
C 694	14	2.3	1648	2	US-08-491-988-13	Sequence 13, Appl	C 767	14	2.3	2182	2	US-08-846-526-8	Sequence 8, Appl
C 695	14	2.3	1662	4	US-09-504-358-5	Sequence 5, Appl	C 768	14	2.3	2193	3	US-09-398-865A-1	Sequence 1, Appl
C 696	14	2.3	1662	4	US-09-554-314-5	Sequence 4, Appl	C 769	14	2.3	2193	4	US-09-710-714-1	Sequence 1, Appl
C 697	14	2.3	1689	1	US-07-991-867B-41	Sequence 41, Appl	C 770	14	2.3	2213	4	US-09-620-312D-799	Sequence 799, App
C 698	14	2.3	1689	2	US-08-544-332-41	Sequence 41, Appl	C 771	14	2.3	2238	2	US-08-919-624-2	Sequence 2, Appl
C 699	14	2.3	1689	2	US-09-370-861A-41	Sequence 41, Appl	C 772	14	2.3	2247	4	US-08-852-824-2	Sequence 2, Appl
C 700	14	2.3	1696	4	US-08-961-527-297	Sequence 297, App	C 773	14	2.3	2295	1	US-08-376-300-3	Sequence 1, Appl
C 701	14	2.3	1710	4	US-09-107-532A-3035	Sequence 3035, Ap	C 774	14	2.3	2295	5	US-09-177-431-3	Sequence 3, Appl
C 702	14	2.3	1711	1	US-08-568-147B-1	Sequence 1, Appl	C 775	14	2.3	2295	5	PCT-US95-16930-3	Sequence 3, Appl
C 703	14	2.3	1713	4	US-08-759-436-1	Sequence 549, App	C 776	14	2.3	2301	4	US-09-134-001C-852	Sequence 852, App
C 704	14	2.3	1722	4	US-09-328-352-549	Sequence 15, Appl	C 777	14	2.3	2340	4	US-09-450-852-3	Sequence 3, Appl
C 705	14	2.3	1725	4	US-08-842-248A-15	Sequence 15, Appl	C 778	14	2.3	2349	4	US-09-489-847-41	Sequence 41, Appl
C 706	14	2.3	1725	4	US-08-842-248A-15	Sequence 15, Appl	C 779	14	2.3	2356	1	US-07-821-716-3	Sequence 3, Appl
C 707	14	2.3	1733	3	US-09-147-522-1	Sequence 1, Appl	C 780	14	2.3	2359	1	US-08-426-169-5	Sequence 5, Appl
C 708	14	2.3	1737	4	US-09-173-151A-1	Sequence 1, Appl	C 781	14	2.3	2359	3	US-09-233-813-5	Sequence 5, Appl
C 709	14	2.3	1739	4	US-09-800-274-3	Sequence 3, Appl	C 782	14	2.3	2359	5	PCT-US95-09470-5	Sequence 5, Appl
C 710	14	2.3	1745	4	US-09-388-349-5	Sequence 2, Appl	C 783	14	2.3	2389	4	US-08-961-083-55	Sequence 55, Appl
C 711	14	2.3	1765	1	US-08-336-778-2	Sequence 2, Appl	C 784	14	2.3	2389	4	US-09-536-784-55	Sequence 55, Appl
C 712	14	2.3	1767	4	US-09-016-434-1345	Sequence 1345, Ap	C 785	14	2.3	2396	4	US-09-221-017B-74	Sequence 74, Appl
C 713	14	2.3	1769	1	US-07-792-865D-3	Sequence 3, Appl	C 786	14	2.3	2405	1	US-08-454-097-30	Sequence 30, Appl
C 714	14	2.3	1784	4	US-09-601-198-21	Sequence 21, Appl	C 787	14	2.3	2405	3	US-08-185-359-30	Sequence 30, Appl
C 715	14	2.3	1785	4	US-09-601-198-156	Sequence 156, App	C 788	14	2.3	2410	2	US-08-780-835B-1	Sequence 1, Appl
C 716	14	2.3	1812	4	US-09-268-347-37	Sequence 37, Appl	C 789	14	2.3	2410	3	US-09-303-268-1	Sequence 1, Appl
C 717	14	2.3	1832	4	US-09-686-583B-42	Sequence 42, Appl	C 790	14	2.3	2410	3	US-09-116-049-1	Sequence 1, Appl
C 718	14	2.3	1832	4	US-09-686-583B-44	Sequence 44, Appl	C 791	14	2.3	2410	4	US-09-884-363-1	Sequence 1, Appl
C 719	14	2.3	1851	4	US-09-608-790-2	Sequence 2, Appl	C 792	14	2.3	2412	4	US-09-253-991A-11898	Sequence 11898, A
C 720	14	2.3	1853	3	US-08-910-864-13	Sequence 13, Appl	C 793	14	2.3	2451	4	US-09-468-656A-9	Sequence 9, Appl
C 721	14	2.3	1893	4	US-09-328-352-112	Sequence 112, Appl	C 794	14	2.3	2465	3	US-08-619-812-5	Sequence 5, Appl
C 722	14	2.3	1912	4	US-09-186-002-17	Sequence 17, Appl	C 795	14	2.3	2478	4	US-09-328-352-390	Sequence 390, App
C 723	14	2.3	1920	4	US-09-108-010B-2	Sequence 2, Appl	C 796	14	2.3	2501	3	US-08-787-739-58	Sequence 58, Appl
C 724	14	2.3	1926	2	US-08-464-517-5	Sequence 5, Appl	C 797	14	2.3	2501	3	US-09-178-115-58	Sequence 58, Appl
C 725	14	2.3	1926	3	US-08-463-772-5	Sequence 5, Appl	C 798	14	2.3	2501	3	US-09-177-776-58	Sequence 58, Appl
C 726	14	2.3	1926	3	PCT-US93-05000-5	Sequence 5, Appl	C 799	14	2.3	2521	4	US-09-620-312D-777	Sequence 777, App
C 727	14	2.3	1947	4	US-09-370-861A-74	Sequence 74, Appl	C 800	14	2.3	2525	3	US-09-342-648-1	Sequence 1, Appl
C 728	14	2.3	1947	4	US-09-328-352-3756	Sequence 3756, Ap	C 801	14	2.3	2553	4	US-09-328-352-2457	Sequence 2457, Ap
C 729	14	2.3	1962	2	US-08-246-361A-5	Sequence 25, Appl	C 802	14	2.3	2571	4	US-09-996-243-318	Sequence 218, App
C 730	14	2.3	1984	1	US-07-885-970A-25	Sequence 25, Appl	C 803	14	2.3	2612	3	US-09-042-785A-3	Sequence 3, Appl
C 731	14	2.3	1985	1	US-08-298-687A-25	Sequence 25, Appl	C 804	14	2.3	2616	4	US-09-620-312D-117	Sequence 117, App
C 732	14	2.3	1985	1	US-08-298-687A-25	Sequence 25, Appl	C 805	14	2.3	2628	2	US-08-696-944-1	Sequence 1, Appl
C 733	14	2.3	1985	1	US-08-298-687A-25	Sequence 25, Appl	C 806	14	2.3	2640	1	US-08-216-971-1	Sequence 1, Appl
C 734	14	2.3	1997	4	US-09-669-731-3	Sequence 3, Appl	C 807	14	2.3	2640	2	US-08-812-979-1	Sequence 12, Appl
C 735	14	2.3	2012	1	US-07-866-560-3	Sequence 3, Appl	C 808	14	2.3	2676	4	US-08-976-259-12	Sequence 3562, Ap
C 736	14	2.3	2012	1	US-08-077-673-3	Sequence 3, Appl	C 809	14	2.3	2679	4	US-09-328-352-3562	Sequence 3, Appl
C 737	14	2.3	2012	1	US-08-478-992-3	Sequence 3, Appl	C 810	14	2.3	2699	4	US-09-336-115C-3	Sequence 3, Appl
C 738	14	2.3	2012	3	US-09-105-298-3	Sequence 7, Appl	C 811	14	2.3	2722	2	US-08-500-857A-7	Sequence 7, Appl
C 739	14	2.3	2012	3	US-08-706-281A-7	Sequence 7, Appl	C 812	14	2.3	2739	4	US-08-184-534A-1C	Sequence 184, App
C 740	14	2.3	2012	4	US-09-097-231-7	Sequence 3, Appl	C 813	14	2.3	2799	4	US-09-134-001C-156	Sequence 156, App
C 741	14	2.3	2012	4	US-09-542-122-3	Sequence 3, Appl	C 814	14	2.3	2799	4	US-08-887-534A-1C	Sequence 44, Appl
C 742	14	2.3	2037	3	US-09-353-099-7	Sequence 14, Appl	C 815	14	2.3	2799	4	US-09-527-431-44	Sequence 44, Appl
C 743	14	2.3	2047	3	US-08-913-942-14	Sequence 1, Appl	C 816	14	2.3	2821	4	US-09-484-970B-44	Sequence 44, Appl
C 744	14	2.3	2065	3	US-08-836-261A-1	Sequence 1, Appl	C 817	14	2.3	2826	4	US-09-390-134B-30	Sequence 30, Appl
C 745	14	2.3	2065	3	US-08-335-865B-8	Sequence 8, Appl	C 818	14	2.3	2838	3	US-08-246-489-1	Sequence 1, Appl
C 746	14	2.3	2073	4	US-09-221-017B-894	Sequence 894, App	C 819	14	2.3	2859	4	US-09-328-352-1485	Sequence 1485, Ap
C 747	14	2.3	2079	4	US-09-268-347-25	Sequence 25, Appl	C 820	14	2.3	2862	4	US-09-443-184-4-16	Sequence 36, Appl
C 748	14	2.3	2107	3	US-09-180-852-1	Sequence 1, Appl	C 821	14	2.3	2880	4	US-09-016-434-1125	Sequence 1125, Ap
C 749	14	2.3	2116	4	US-09-484-970B-122	Sequence 122, App	C 822	14	2.3	2887	3	US-09-183-253-1	Sequence 1, Appl
C 750	14	2.3	2126	4	US-09-134-001C-2519	Sequence 2519, Ap	C 823	14	2.3	2906	4	US-09-996-243-500	Sequence 500, App
C 751	14	2.3	2126	2	US-08-545-745-1	Sequence 1, Appl	C 824	14	2.3	2907	3	US-08-816-346-1	Sequence 1, Appl
C 752	14	2.3	2133	4	US-09-328-352-424	Sequence 424, App	C 825	14	2.3	2907	3	US-08-816-346-55	Sequence 55, Appl
C 753	14	2.3	2143	4	US-09-205-258-235	Sequence 235, App	C 826	14	2.3	2907	3	US-09-335-411-1	Sequence 1, Appl
C 754	14	2.3	2156	4	US-08-965-762-16	Sequence 16, Appl	C 827	14	2.3	2920	4	US-09-335-411-55	Sequence 55, Appl
C 755	14	2.3	2156	4	US-09-911-927-18	Sequence 18, Appl	C 828	14	2.3	2920	4	US-09-620-312D-1084	Sequence 1084, Ap
C 756	14	2.3	2156	4	US-09-911-927-18	Sequence 18, Appl	C 829	14	2.3	3001	4	US-09-539-333D-129	Sequence 129, App
C 757	14	2.3	2156	4	US-09-911-882-16	Sequence 16, Appl	C 830	14	2.3	3001	4	US-09-539-333D-184	Sequence 184, App
C 757	14	2.3	2156	4	US-09-911-882-18	Sequence 18, Appl						US-09-539-333D-195	Sequence 195, App

831	14	2.3	3001	4	US-09-539-333D-199	Sequence 199, App	C 904	14	2.3	3834	4	US-09-620-312D-933	Sequence 933, App
832	14	2.3	3030	4	US-09-268-347-29	Sequence 29, App1	C 905	14	2.3	3865	1	US-08-832-883-48	Sequence 48, App1
C 833	14	2.3	3032	4	US-08-990-140-1	Sequence 1, Appli	C 906	14	2.3	3865	1	US-08-832-883-48	Sequence 48, App1
C 834	14	2.3	3032	4	US-09-546-238-1	Sequence 1, Appli	C 907	14	2.3	3865	2	US-08-832-877-48	Sequence 48, App1
835	14	2.3	3036	4	US-09-268-347-23	Sequence 21, Appli	C 908	14	2.3	3865	2	US-08-832-877-48	Sequence 48, App1
836	14	2.3	3063	4	US-08-184-009-159	Sequence 169, App	C 909	14	2.3	3997	2	US-08-821-994-72	Sequence 72, App1
837	14	2.3	3063	2	US-08-458-356-169	Sequence 169, App	C 910	14	2.3	4016	1	US-08-410-540-3	Sequence 3, Appli
838	14	2.3	3063	4	US-08-460-736-169	Sequence 169, App	C 911	14	2.3	4035	4	US-09-016-434-1369	Sequence 1369, App
839	14	2.3	3063	4	US-09-535-370-169	Sequence 169, App	C 912	14	2.3	4080	1	US-08-375-300-1	Sequence 1, Appli
840	14	2.3	3115	4	US-09-702-705-802	Sequence 802, App	C 913	14	2.3	4080	3	US-09-177-431-1	Sequence 1, Appli
841	14	2.3	3115	4	US-09-736-457-802	Sequence 802, App	C 914	14	2.3	4080	5	PCT-US95-16330-1	Sequence 1, Appli
842	14	2.3	3129	4	US-09-904-615-18	Sequence 18, App1	C 915	14	2.3	4104	3	US-08-881-706-1	Sequence 1, Appli
843	14	2.3	3144	4	US-08-961-527-224	Sequence 224, App	C 916	14	2.3	4138	1	US-08-447-411-15	Sequence 75, Appli
844	14	2.3	3162	4	US-09-221-017B-766	Sequence 766, App	C 917	14	2.3	4138	2	US-08-662-227-53	Sequence 33, App1
845	14	2.3	3165	4	US-09-601-198-102	Sequence 102, App	C 918	14	2.3	4138	4	US-09-017-947-33	Sequence 33, App1
C 846	14	2.3	3177	4	US-09-601-198-102	Sequence 102, App	C 919	14	2.3	4148	4	US-09-435-019-13	Sequence 13, App1
C 847	14	2.3	3177	3	US-09-134-513-1	Sequence 1, Appli	C 920	14	2.3	4148	4	US-09-435-019-15	Sequence 15, App1
C 848	14	2.3	3191	3	US-08-675-816-3	Sequence 3, Appli	C 921	14	2.3	4160	4	US-09-134-218-1	Sequence 1, Appli
C 849	14	2.3	3195	4	US-09-527-058-3	Sequence 3, Appli	C 922	14	2.3	4161	4	US-09-252-991A-12016	Sequence 12016, A
C 850	14	2.3	3245	1	US-07-935-311A-3	Sequence 3, Appli	C 923	14	2.3	4203	2	US-08-288-630-3	Sequence 3, App1
C 851	14	2.3	3245	1	US-08-368-079-3	Sequence 3, Appli	C 924	14	2.3	4223	3	US-09-541-782-5	Sequence 5, App1
C 852	14	2.3	3245	5	PCT-US93-07996-3	Sequence 3, Appli	C 925	14	2.3	4223	4	US-09-723-820-5	Sequence 5, App1
C 853	14	2.3	3300	4	US-09-336-643A-82	Sequence 82, App1	C 926	14	2.3	4248	3	US-08-678-614-1	Sequence 1, Appli
C 854	14	2.3	3300	4	US-09-620-312D-456	Sequence 456, App	C 927	14	2.3	4285	4	US-09-410-464-1	Sequence 1, Appli
C 855	14	2.3	3312	4	US-09-601-198-58	Sequence 58, App1	C 928	14	2.3	4301	4	US-08-121-446-3	Sequence 3, App1
C 856	14	2.3	3331	3	US-08-864-038A-2	Sequence 2, Appli	C 929	14	2.3	4398	1	US-08-961-527-293	Sequence 293, App
857	14	2.3	3331	3	US-08-864-038A-4	Sequence 4, Appli	C 930	14	2.3	4406	4	US-08-233-788A-39	Sequence 39, App1
C 858	14	2.3	3340	4	US-09-021-560-1	Sequence 1, Appli	C 931	14	2.3	4443	4	US-09-425-453A-1	Sequence 1, Appli
C 859	14	2.3	3342	4	US-09-620-312D-449	Sequence 449, App	C 932	14	2.3	4443	4	US-09-425-453A-3	Sequence 3, App1
C 860	14	2.3	3414	1	US-08-764-100-17	Sequence 17, App1	C 933	14	2.3	4443	4	US-09-425-453A-5	Sequence 5, App1
C 861	14	2.3	3414	1	US-08-764-100-21	Sequence 21, App1	C 934	14	2.3	4443	4	US-09-425-453A-7	Sequence 7, App1
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C 863	14	2.3	3426	1	US-08-234-939-1	Sequence 1, Appli	C 936	14	2.3	4443	4	US-09-425-453A-11	Sequence 11, App1
C 864	14	2.3	3426	1	US-08-558-885-1	Sequence 1, Appli	C 937	14	2.3	4443	4	US-09-425-453A-13	Sequence 13, App1
C 865	14	2.3	3426	3	US-08-654-025-6	Sequence 6, App1	C 938	14	2.3	4443	4	US-09-425-453A-15	Sequence 15, App1
C 866	14	2.3	3460	4	US-09-620-312D-666	Sequence 666, App	C 939	14	2.3	4443	4	US-09-425-453A-17	Sequence 17, App1
C 867	14	2.3	3465	4	US-09-134-001C-591	Sequence 591, App	C 940	14	2.3	4443	4	US-09-425-453A-19	Sequence 19, App1
C 868	14	2.3	3468	1	US-09-221-017B-893	Sequence 893, App	C 941	14	2.3	4451	3	US-08-717-294-42	Sequence 42, App1
C 869	14	2.3	3487	4	US-08-410-540-4	Sequence 4, Appli	C 942	14	2.3	4560	3	US-09-256-703-1	Sequence 1, Appli
C 870	14	2.3	3497	4	US-09-495-052-58	Sequence 58, App1	C 943	14	2.3	4576	1	US-08-832-883-49	Sequence 49, App1
871	14	2.3	3507	1	US-08-315-468-3	Sequence 3, Appli	C 944	14	2.3	4576	2	US-08-832-877-49	Sequence 49, App1
C 872	14	2.3	3511	4	US-09-453-702B-187	Sequence 187, App	C 945	14	2.3	4637	4	US-09-702-705-604	Sequence 804, App
873	14	2.3	3520	1	US-08-424-788-3	Sequence 1, Appli	C 946	14	2.3	4637	4	US-09-736-457-804	Sequence 804, App
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875	14	2.3	3520	2	US-08-477-166-3	Sequence 3, Appli	C 948	14	2.3	4863	4	US-09-618-425-8	Sequence 8, App1
876	14	2.3	3520	2	US-08-472-097-3	Sequence 3, Appli	C 949	14	2.3	4874	4	US-09-484-970B-36	Sequence 36, App1
877	14	2.3	3520	2	US-08-439-672-3	Sequence 3, Appli	C 950	14	2.3	4875	1	US-08-460-739-1	Sequence 1, App1
878	14	2.3	3520	5	PCT-US93-11638-3	Sequence 3, Appli	C 951	14	2.3	4895	4	US-09-426-568A-3	Sequence 3, App1
879	14	2.3	3532	3	US-08-787-739-90	Sequence 90, App1	C 952	14	2.3	4935	2	US-08-631-097-3	Sequence 3, App1
880	14	2.3	3532	3	US-09-178-115-90	Sequence 90, App1	C 953	14	2.3	4951	2	US-08-867-030B-5	Sequence 5, App1
881	14	2.3	3532	3	US-09-177-776-90	Sequence 90, App1	C 954	14	2.3	4951	5	PCT-US95-06119-5	Sequence 5, App1
882	14	2.3	3534	4	US-09-134-001C-2269	Sequence 2269, App	C 955	14	2.3	4970	1	US-08-764-100-14	Sequence 14, App1
C 883	14	2.3	3531	1	US-08-198-446B-18	Sequence 18, App1	C 956	14	2.3	4970	1	US-08-764-100-20	Sequence 20, App1
C 884	14	2.3	3551	2	US-08-870-693-18	Sequence 18, App1	C 957	14	2.3	5011	1	US-08-141-893-1	Sequence 1, App1
C 885	14	2.3	3612	4	US-09-068-506-2	Sequence 2, Appli	C 958	14	2.3	5011	1	US-08-463-092B-1	Sequence 1, App1
C 886	14	2.3	3633	4	US-09-221-017B-362	Sequence 362, App	C 959	14	2.3	5011	1	US-08-463-092B-3	Sequence 3, App1
887	14	2.3	3636	4	US-09-328-352-3841	Sequence 3841, App	C 960	14	2.3	5011	2	US-08-462-109A-1	Sequence 1, App1
C 888	14	2.3	3690	4	US-09-016-434-1234	Sequence 1234, App	C 961	14	2.3	5011	2	US-08-462-109A-3	Sequence 3, App1
C 889	14	2.3	3701	3	US-08-845-258-10	Sequence 10, App1	C 962	14	2.3	5011	2	US-08-460-907B-1	Sequence 1, App1
C 890	14	2.3	3701	3	US-08-990-571-10	Sequence 10, App1	C 963	14	2.3	5011	2	US-08-460-907B-3	Sequence 3, App1
C 891	14	2.3	3701	3	US-08-723-142A-10	Sequence 10, App1	C 964	14	2.3	5011	3	US-08-463-179A-1	Sequence 1, App1
C 892	14	2.3	3701	4	US-09-528-784A-10	Sequence 10, App1	C 965	14	2.3	5011	3	US-08-463-179A-3	Sequence 3, App1
C 893	14	2.3	3701	4	US-09-583-545-1	Sequence 1, Appli	C 966	14	2.3	5011	3	US-08-461-384B-1	Sequence 1, App1
894	14	2.3	3701	4	US-09-617-594A-5	Sequence 5, Appli	C 967	14	2.3	5011	3	US-08-461-384B-3	Sequence 3, App1
C 895	14	2.3	3701	4	US-09-569-098A-5	Sequence 5, Appli	C 968	14	2.3	5011	3	US-08-407-207A-1	Sequence 1, App1
896	14	2.3	3706	2	US-08-566-398-59	Sequence 59, App1	C 969	14	2.3	5024	4	US-09-307-143-1	Sequence 1, App1
897	14	2.3	3706	2	US-08-658-665-63	Sequence 63, App1	C 970	14	2.3	5111	4	US-09-004-848-118	Sequence 118, App
898	14	2.3	3706	3	US-08-796-101-27	Sequence 27, App1	C 971	14	2.3	5113	4	US-09-336-946B-3	Sequence 3, App1
899	14	2.3	3706	3	US-09-085-273-63	Sequence 63, App1	C 972	14	2.3	5140	4	US-09-333-214-2	Sequence 2, App1
C 900	14	2.3	3718	4	US-09-424-283-6	Sequence 63, App1	C 973	14	2.3	5222	4	US-09-336-946B-68	Sequence 68, App1
C 901	14	2.3	3791	4	US-09-149-476-216	Sequence 216, App	C 974	14	2.3	5240	4	US-09-171-337A-2	Sequence 2, App1
C 902	14	2.3	3812	1	US-08-188-582-19	Sequence 19, App1	C 975	14	2.3	5240	4	US-09-631-022-2	Sequence 2, App1
C 903	14	2.3	3812	1	US-08-646-715-19	Sequence 19, App1	C 976	14	2.3	5261	1	US-08-045-806-3	Sequence 3, App1

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c 977      14      2.3      5261 1 US-08-366-051B-3 Sequence 3, Appl1
c 978      14      2.3      5303 4 US-08-971-395-4 Sequence 4, Appl1
c 979      14      2.3      5305 4 US-08-961-527-135 Sequence 135, App
c 980      14      2.3      5401 3 US-09-269-040-1 Sequence 1, Appl1
c 981      14      2.3      5407 3 US-09-269-040-7 Sequence 7, Appl1
c 982      14      2.3      5416 4 US-09-284-926-8 Sequence 8, Appl1
c 983      14      2.3      5433 2 US-08-929-329-1 Sequence 1, Appl1
c 984      14      2.3      5543 2 US-08-687-080-101 Sequence 101, App
c 985      14      2.3      5574 1 US-08-450-257-22 Sequence 22, Appl
c 986      14      2.3      5574 1 US-08-450-246-22 Sequence 22, Appl
c 987      14      2.3      5574 1 US-08-450-098-22 Sequence 22, Appl
c 988      14      2.3      5574 1 US-08-451-233-22 Sequence 22, Appl
c 989      14      2.3      5574 1 US-08-450-236-22 Sequence 22, Appl
c 990      14      2.3      5581 4 US-08-235-403-22 Sequence 22, Appl
c 991      14      2.3      5581 4 US-08-973-544-1 Sequence 1, Appl1
c 992      14      2.3      5635 3 US-08-136-742A-3 Sequence 3, Appl1
c 993      14      2.3      5635 3 US-09-248-026-3 Sequence 3, Appl1
c 994      14      2.3      5635 5 PCT-US93-11667-3 Sequence 3, Appl1
c 995      14      2.3      5706 4 US-09-738-946-11 Sequence 11, Appl
c 996      14      2.3      5757 4 US-09-336-946B-11 Sequence 1, Appl1
c 997      14      2.3      5886 3 US-08-810-712-9 Sequence 9, Appl1
c 998      14      2.3      5943 1 US-08-206-176-1 Sequence 1, Appl1
c 999      14      2.3      5977 3 US-09-024-020B-1 Sequence 1, Appl1
c1000      14      2.3      5977 4 US-09-425-043-1 Sequence 1, Appl1

```

ALIGNMENTS

```

RESULT 1
US-09-495-050A-28
; Sequence 28, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 647628CT1
US-09-495-050A-28

Query Match      3.1%; Score 19; DB 4; Length 948;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 ACCTATTTTATGATGCCA 279
DB      678 ACCTATTTTATGATGCCA 696

RESULT 2
US-09-422-978-2313/c
; Sequence 2313, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI

```

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; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2313
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-10364-331 : polymorphic base A or G
US-09-422-978-2313

Query Match      2.9%; Score 18; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      162 TTTGAAACAATTTCTA 179
DB      21 TTTGAAACAATTTCTA 4

```

```

RESULT 3
US-08-232-463-29/c
; Sequence 29, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: oligonucleotide II
US-08-232-463-29

Query Match 2.9%; Score 18; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 35 TTCTACTATATTTTACA 18

RESULT 4

US-08-232-463-38/c
Sequence 38, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: sp11(4)
US-08-232-463-38

Query Match 2.9%; Score 18; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 35 TTCTACTATATTTTACA 18

RESULT 5

US-08-232-463-44/c
Sequence 44, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: Plim
US-08-232-463-44

Query Match 2.9%; Score 18; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTCTACTATATTTTACA 192
|||||
Db 34 TTCTACTATATTTTACA 17

RESULT 6

US-08-232-463-45/c
Sequence 45, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA


```
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: SP11
US-08-232-463-45
```

```
Query Match      2.9%; Score 18; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      175 TTCTACTATATTTTACCA 192
Db      35 TTCTACTATATTTTACCA 18
```

```
RESULT 7
US-08-232-463-43/C
Sequence 43, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
```

```
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: P11wc
US-08-232-463-43
```

```
Query Match      2.9%; Score 18; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      175 TTCTACTATATTTTACCA 192
Db      29 TTCTACTATATTTTACCA 12
```

```
RESULT 8
US-09-439-313-535/C
Sequence 535, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-535
```

```
Query Match      2.9%; Score 18; DB 4; Length 6082;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      114 AGCAGGATGCTGGGGCT 131
Db      107 AGCAGGATGCTGGGGCT 90
```

```
RESULT 9
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
```


TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpc-Fls
US-08-232-463-14

Query Match 2.9%; Score 18; DB 1; Length 7218;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTTACA 192
|||||
DB 1599 TTCTACTATATTTTACA 1582

RESULT 10
US-08-232-463-2/C
Sequence 2, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTKm-sp11
US-08-232-463-2

Query Match 2.9%; Score 18; DB 1; Length 8313;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTTACA 192
|||||
DB 4160 TTCTACTATATTTTACA 4143

RESULT 11
US-08-480-882B-3
Sequence 3, Application US/08480882B
Patent No. 5656275
GENERAL INFORMATION:
APPLICANT: WASKOEN, TERRI
APPLICANT: CHAVEZ, LLOYD
APPLICANT: CHU, HSIEN-JUE
TITLE OF INVENTION: RECOMBINANT RACCOON FOX VIRUSES
TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
TITLE OF INVENTION: INFECTIOUS PERITONITIS VIRUS DISEASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Darby & Darby, P.C.
STREET: 805 Third Avenue 27th Floor
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,882B
FILING DATE: 07-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,516
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 0632/08669
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2125277700
TELEFAX: 2127536237

```
TELEX: 236687
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Feline infectious peritonitis virus
; IMMEDIATE SOURCE:
; CLONE: psc11f1
US-08-480-882B-3

Query Match      2.9%; Score 18; DB 1; Length 8710;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      175 TTCTACTATATTTTACA 192
        |||||
Db      6148 TTCTACTATATTTTACA 6165

RESULT 12
US-08-480-210-3
; Sequence 3, Application US/08480210
; Patent No. 5770211
; GENERAL INFORMATION:
; APPLICANT: MASMOEN, TERRI
; APPLICANT: CHAVEZ, LLOYD
; APPLICANT: CHU, HSIEN-JUE
; TITLE OF INVENTION: RECOMBINANT RACCOON POX VIRUSES
; TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
; TITLE OF INVENTION: INFECTIOUS PERITONITIS VIRUS DISEASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue 27th Floor
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,210
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,516
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0632/18669-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2125277700
; TELEFAX: 2127536237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8710 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Feline infectious peritonitis virus
; IMMEDIATE SOURCE:
; CLONE: psc11f1
```

```
US-08-480-210-3

Query Match      2.9%; Score 18; DB 1; Length 8710;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      175 TTCTACTATATTTTACA 192
        |||||
Db      6148 TTCTACTATATTTTACA 6165

RESULT 13
US-08-480-882B-4
; Sequence 4, Application US/08480882B
; Patent No. 5656275
; GENERAL INFORMATION:
; APPLICANT: MASMOEN, TERRI
; APPLICANT: CHAVEZ, LLOYD
; APPLICANT: CHU, HSIEN-JUE
; TITLE OF INVENTION: RECOMBINANT RACCOON POX VIRUSES
; TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
; TITLE OF INVENTION: INFECTIOUS PERITONITIS VIRUS DISEASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue 27th Floor
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,882B
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,516
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0632/08669
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2125277700
; TELEFAX: 2127536237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9019 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Feline immunodeficiency virus
; IMMEDIATE SOURCE:
; CLONE: psc11e1
US-08-480-882B-4

Query Match      2.9%; Score 18; DB 1; Length 9019;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      175 TTCTACTATATTTTACA 192
        |||||
Db      6147 TTCTACTATATTTTACA 6164

RESULT 14
```

US-08-480-210-4
; Sequence 4, Application US/08480210
; Patent No. 5770211
; GENERAL INFORMATION:
; APPLICANT: WASMOEN, TERRI
; APPLICANT: CHAVEZ, LLOYD
; APPLICANT: CHU, HSIEH-JUE
; TITLE OF INVENTION: RECOMBINANT RACCOON POX VIRUSES
; TITLE OF INVENTION: AND THEIR USE AS AN EFFECTIVE VACCINE AGAINST FELINE
; TITLE OF INVENTION: INFECTIOUS PERITONITIS VIRUS DISEASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue 27th Floor
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,210
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,516
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0632/18669-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2125277700
; TELEFAX: 2127536237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9019 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Feline immunodeficiency virus
; IMMEDIATE SOURCE:
; CLONE: psc11e1
; US-08-480-210-4

Query Match 2.9%; Score 18; DB 1; Length 9019;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 175 TTCTACTATATTTTACA 192
|||||
Db 6147 TTCTACTATATTTTACA 6164

RESULT 15
US-08-232-463-3/c
; Sequence 3, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9454 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTKm-VtkA
; US-08-232-463-3

Query Match 2.9%; Score 18; DB 1; Length 9454;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 175 TTCTACTATATTTTACA 192
|||||
Db 5301 TTCTACTATATTTTACA 5284

RESULT 16
US-08-232-463-4/c
; Sequence 4, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313

FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTKm-VVekb
US-08-232-463-4

Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTTACA 192
DB 5301 TTCTACTATATTTTACA 5284

RESULT 17
US-08-232-463-16
Sequence 16, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEITFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9917 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-spl1
US-08-232-463-16

Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTTACA 192
DB 4329 TTCTACTATATTTTACA 4346

RESULT 18
US-09-146-053-3/c
Sequence 3, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human Aminopeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
CURRENT FILING DATE: 1998-09-02
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 50000
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-053-3

Query Match
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 495 AGAGTTTCAAACTTTT 512
DB 39492 AGAGTTTCAAACTTTT 39475

RESULT 19
US-09-733-294A-30
Sequence 30, Application US/09733294A
Patent No. 6492171
GENERAL INFORMATION:
APPLICANT: Brett P. Montz
APPLICANT: William Gaarde
APPLICANT: Susan M. Freiler
APPLICANT: Edward V. Mancewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0527
CURRENT APPLICATION NUMBER: US/09/733,294A
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/572,423
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 30
LENGTH: 51552
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: (1)...(11492)
OTHER INFORMATION: exon 1
NAME/KEY: intron
LOCATION: (11493)...(11596)
OTHER INFORMATION: intron 1

NAME/KEY: exon
 LOCATION: (11597)...(12950)
 OTHER INFORMATION: exon 2
 NAME/KEY: intron
 LOCATION: (12951)...(21566)
 OTHER INFORMATION: intron 2
 NAME/KEY: exon
 LOCATION: (21567)...(21762)
 OTHER INFORMATION: exon 3
 NAME/KEY: intron
 LOCATION: (21763)...(23851)
 OTHER INFORMATION: intron 3
 NAME/KEY: exon
 LOCATION: (23852)...(24032)
 OTHER INFORMATION: exon 4
 NAME/KEY: intron
 LOCATION: (24033)...(24719)
 OTHER INFORMATION: intron 4
 NAME/KEY: exon
 LOCATION: (24720)...(24899)
 OTHER INFORMATION: exon 5
 NAME/KEY: intron
 LOCATION: (24900)...(25393)
 OTHER INFORMATION: intron 5
 NAME/KEY: exon
 LOCATION: (25394)...(25549)
 OTHER INFORMATION: exon 6
 NAME/KEY: intron
 LOCATION: (25550)...(30196)
 OTHER INFORMATION: intron 6
 NAME/KEY: exon
 LOCATION: (30195)...(30292)
 OTHER INFORMATION: exon 7
 NAME/KEY: intron
 LOCATION: (30293)...(31272)
 OTHER INFORMATION: intron 7
 NAME/KEY: exon
 LOCATION: (31273)...(31358)
 OTHER INFORMATION: exon 8
 NAME/KEY: intron
 LOCATION: (31359)...(33843)
 OTHER INFORMATION: intron 8
 NAME/KEY: unsure
 LOCATION: 31450
 OTHER INFORMATION: unknown
 NAME/KEY: exon
 LOCATION: (33844)...(33957)
 OTHER INFORMATION: exon 9
 NAME/KEY: intron
 LOCATION: (33958)...(35941)
 OTHER INFORMATION: intron 9
 NAME/KEY: exon
 LOCATION: (35942)...(36013)
 OTHER INFORMATION: exon 10
 NAME/KEY: intron
 LOCATION: (36014)...(37884)
 OTHER INFORMATION: intron 10
 NAME/KEY: exon
 LOCATION: (37885)...(38073)
 OTHER INFORMATION: exon 11
 NAME/KEY: intron
 LOCATION: (38074)...(41874)
 OTHER INFORMATION: intron 11
 NAME/KEY: exon
 LOCATION: (41875)...(42001)
 OTHER INFORMATION: exon 12
 NAME/KEY: intron
 LOCATION: (42002)...(42881)
 OTHER INFORMATION: intron 12
 NAME/KEY: exon
 LOCATION: (42882)...(42943)
 OTHER INFORMATION: exon 13
 NAME/KEY: intron

LOCATION: (42944)...(46129)
 OTHER INFORMATION: intron 13
 NAME/KEY: exon
 LOCATION: (46130)...(46254)
 OTHER INFORMATION: exon 14
 NAME/KEY: intron
 LOCATION: (46255)...(47035)
 OTHER INFORMATION: intron 14
 NAME/KEY: exon
 LOCATION: (47036)...(47173)
 OTHER INFORMATION: exon 15
 NAME/KEY: intron
 LOCATION: (47174)...(47709)
 OTHER INFORMATION: intron 15
 NAME/KEY: exon
 LOCATION: (47710)...(50544)
 OTHER INFORMATION: exon 16
 US-09-733-294A-30

Query Match 2.9%; Score 18; DB 4; Length 51552;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GCAGCAGGATGCTGGCG 129
 Db 48650 GCAGCAGGATGCTGGCG 48667

RESULT 20
 US-08-998-416-574
 Sequence 574, Application US/08998416
 Patent No. 6239264
 GENERAL INFORMATION:
 APPLICANT: Philippsen, Peter
 APPLICANT: Pohmann, Rainer
 APPLICANT: Steiner, Sabine
 APPLICANT: Mohr, Christine
 APPLICANT: Wendland, Jurgen
 APPLICANT: Knechtle, Philipp
 APPLICANT: Reibschung, Corinne
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII
 TITLE OF INVENTION: AND USES THEREOF
 NUMBER OF SEQUENCES: 1152
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: No. 6239264artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: No. 6239264th Carolina
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/998,416
 FILING DATE: 24-DEC-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: CH 0016/97
 FILING DATE: 31-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 574:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 753 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1397RP
US-08-998-416-574

Query Match 2.7%; Score 17; DB 3; Length 753;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 TATTATTATGATGCCA 280
DB 286 TATTATTATGATGCCA 302

RESULT 21

US-09-107-532A-2443
Sequence 2443; Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Daneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2443:
SEQUENCE CHARACTERISTICS:
LENGTH: 876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...876
SEQUENCE DESCRIPTION: SEQ ID NO: 2443:
US-09-107-532A-2443
Query Match 2.7%; Score 17; DB 4; Length 876;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 TAGGATATGTCATAT 480
DB 617 TAGGATATGTCATAT 633

RESULT 22

US-09-016-434-982
Sequence 982; Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 982:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGAST01
CLONE: 873352
US-09-016-434-982
Query Match 2.7%; Score 17; DB 4; Length 1337;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 TTTGAACAATTTCT 178
DB 406 TTTGAACAATTTCT 422

RESULT 23
US-09-329-633A-1
Sequence 1; Application US/09329633A
Patent No. 6252050
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntcharapai, Anan
APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
FILE REFERENCE: P1468R1 (REVISED)

```

; CURRENT APPLICATION NUMBER: US/09/329,633A
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/089,253
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO: 1
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: human
US-09-329-633A-1

Query Match      2.7%; Score 17; DB 3; Length 1799;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      230 ATGCTTATTTATTTAT 246
        |||||
Db      1684 ATGCTTATTTATTTAT 1700

RESULT 24
US-09-079-029-2
; Sequence 2, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1799 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-079-029-2

Query Match      2.7%; Score 17; DB 4; Length 1799;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      230 ATGCTTATTTATTTAT 246
        |||||
Db      1684 ATGCTTATTTATTTAT 1700

RESULT 25
US-09-453-702B-188
```

```

; Sequence 188, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blatner, Frederick R.
; APPLICANT: Burland, Nicole T.
; APPLICANT: Perna, Nicole T.
; APPLICANT: Plunkett, Guy
; APPLICANT: Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Plunkett Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1819
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-09-453-702B-188

Query Match      2.7%; Score 17; DB 4; Length 1819;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      159 TCATTGAAACATTT 175
        |||||
Db      82 TCATTGAAACATTT 98

RESULT 26
US-08-915-795-4
; Sequence 4, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
; APPLICANT: Marc G. ACHEN
; APPLICANT: Andrew F. WILKS
; APPLICANT: Steven A. STACKER
; APPLICANT: Karl ALITALO
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKewon, Edwards & Lenahan P.L.L.C.
; STREET: 1200 G Street, NW, Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: United States of America
; ZIP: 20005
```

```
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: Patent Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/08/915,795
/
/ FILING DATE:
/
/ CLASSIFICATION: 536
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: EVANS, Joseph D.
/
/ REGISTRATION NUMBER: 26,269
/
/ REFERENCE/DOCKET NUMBER: 1064/42983
/
/ TELECOMMUNICATION INFORMATION:
/
/ TELEPHONE: (202) 628-8800
/
/ TELEFAX: (202) 628-8844
/
/ TELEX: N/A
/
/ INFORMATION FOR SEQ ID NO: 4:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 2029 base pairs
/
/ TYPE: nucleic acid
/
/ STRANDEDNESS: single
/
/ TOPOLOGY: linear
/
/ MOLECULAR TYPE: cDNA
/
/ HYPOTHETICAL: NO
/
/ ORIGINAL SOURCE:
/
/ TISSUE TYPE: Human Lung
/
/ US-08-915-795-4
```

```
Query Match          2.7%; Score 17; DB 3; Length 2029;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      162 TTTTGAACAATTCT 178
        |||||||
Db      341 TTTTGAACAATTCT 357
```

```
RESULT 27
US-09-134-001C-1659
/ Sequence 1659, Application US/09134001C
/ Patent No. 6380370
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC-007
/ CURRENT APPLICATION NUMBER: US/09/134,001C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ PRIOR FILING DATE: 1997-08-14
/ NUMBER OF SEQ ID NOS: 5674
/ SEQ ID NO 1659
/ LENGTH: 2661
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
/ US-09-134-001C-1659
```

```
Query Match          2.7%; Score 17; DB 4; Length 2661;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      161 ATTTGAACAATTTC 177
        |||||||
Db      1835 ATTTGAACAATTTC 1851
```

```
RESULT 28
US-09-333-593A-1
/ Sequence 1, Application US/09333593A
/ Patent No. 6313269
```

```
/
/ GENERAL INFORMATION:
/
/ APPLICANT: DEEN, KEITH C.
/
/ APPLICANT: YOUNG, PETER R.
/
/ APPLICANT: MARSHALL, LISA A.
/
/ APPLICANT: ROSHAK, AMY K.
/
/ APPLICANT: TAN, KONG B.
/
/ APPLICANT: TRUNEH, ALEMSEGED
/
/ TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
/
/ TITLE OF INVENTION: TR6
/
/ FILE REFERENCE: GH-50008-2
/
/ CURRENT APPLICATION NUMBER: US/09/333,593A
/
/ CURRENT FILING DATE: 1999-06-15
/
/ PRIOR APPLICATION NUMBER: 08/916,625
/
/ PRIOR FILING DATE: 1997-08-22
/
/ PRIOR APPLICATION NUMBER: 08/853,684
/
/ PRIOR FILING DATE: 1997-05-09
/
/ PRIOR APPLICATION NUMBER: 60/041,230
/
/ PRIOR FILING DATE: 1997-03-14
/
/ NUMBER OF SEQ ID NOS: 8
/
/ SOFTWARE: FastSeq for Windows Version 3.0
/
/ SEQ ID NO 1
/
/ LENGTH: 3881
/
/ TYPE: DNA
/
/ ORGANISM: HOMO SAPIENS
/
/ FEATURE:
/
/ NAME/KEY: UNSURE
/
/ LOCATION: (3538) (3598) (3601) (3607) (3608) (3619) (3632) (3659) (3686) (3690)
/
/ US-09-333-593A-1
```

```
Query Match          2.7%; Score 17; DB 4; Length 3881;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      230 ATGCTTTATTATTAT 246
        |||||||
Db      1638 ATGCTTTATTATTAT 1654
```

```
RESULT 29
US-09-620-312D-156/C
/ Sequence 156, Application US/09620312D
/ Patent No. 6569662
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Asundi, Vinod
/ APPLICANT: Zhang, Jie
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Yang, Yonghong
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Zhou, Ping
/ APPLICANT: Ma, Yundong
/ APPLICANT: Wang, Duntui
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: John Tillinghast
/ APPLICANT: Drmanac, Radoje T.
/ TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 764CIP28
/ CURRENT APPLICATION NUMBER: US/09/620,312D
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: 09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ NUMBER OF SEQ ID NOS: 1105
/ SOFTWARE: pc_fl_genes Version 1.0
/ SEQ ID NO 156
/ LENGTH: 4053
```


TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (409)..(3819)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(4053)
OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-156

Query Match 2.7%; Score 17; DB 4; Length 4053;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 534 TTCAGTGTGCAGATT 550
DB 513 TTCAGTGTGCAGATT 497

RESULT 30

US-08-400-159-1/c
Sequence 1, Application US/08400159
Patent No. 5869282
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
FILING DATE: 07-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 442..4656
US-08-400-159-1
Query Match 2.7%; Score 17; DB 2; Length 5561;

Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 373 AAATTATATATATAA 389
DB 5499 AAATTATATATATAA 5483

RESULT 31

US-08-611-729A-1/c
Sequence 1, Application US/08611729A
Patent No. 6004924
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A
FILING DATE: 06-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5561 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 442..4653
US-08-611-729A-1
Query Match 2.7%; Score 17; DB 3; Length 5561;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 373 AAATTATATATATAA 389
DB 5499 AAATTATATATATAA 5483

RESULT 32

US-08-961-527-198
Sequence 198, Application US/08961527
Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunesch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 331
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 6846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-198

Query Match 2.7%; Score 17; DB 4; Length 6846;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 462 TATAGTATTGTTCCAT 478
|||||
Db 1806 TATAGTATTGTTCCAT 1822

RESULT 33
US-08-287-959-2
Sequence 2, Application US/08287959
GENERAL INFORMATION:
APPLICANT: Weisbach, Lawrence
APPLICANT: Bernards, Andre
APPLICANT: Settleman, Jeffrey
TITLE OF INVENTION: GAP-RELATED GENE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,959
FILING DATE: August 9, 1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/181001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7573 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-287-959-2

Query Match 2.7%; Score 17; DB 1; Length 7573;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 AGAGTAGCTATTAT 271
|||||
Db 280 AGAGTAGCTATTAT 296

RESULT 34
US-09-759-359A-3
Sequence 3, Application US/09759359A
Patent No. 6492153
GENERAL INFORMATION:
APPLICANT: ABU-THREIDH, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINSE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01043
CURRENT APPLICATION NUMBER: US/09/759,359A
CURRENT FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 90541
TYPE: DNA
ORGANISM: Human
US-09-759-359A-3

Query Match 2.7%; Score 17; DB 4; Length 90541;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 TGTACAGTTGTGCAT 337
|||||
Db 19972 TGTACAGTTGTGCAT 19988

RESULT 35
US-09-798-096-10/c
Sequence 10, Application US/09798096
Patent No. 6393578
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-798-096-10

Query Match 2.7%; Score 17; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 278 CAATATTACTTTTATT 294
|||||
Db 18670 CAATATTACTTTTATT 18654

RESULT 36

US-09-585-858-1/c
; Sequence 1, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigridur Hjorleifsdottir
; APPLICANT: Gudmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Avarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 129908
; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-09-585-858-1

Query Match 2.7%; Score 17; DB 4; Length 129908;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 423 ACTGTTCGACTTTTAC 439
|||||
Db 32762 ACTGTTCGACTTTTAC 32746

RESULT 37

US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs

TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 2.7%; Score 17; DB 4; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 234 TTTATTATTATGTTG 250
|||||
Db 466814 TTTATTATTATGTTG 466830

RESULT 38

US-09-643-990A-1
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville,
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,990A
; FILING DATE: 23-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 2.7%; Score 17; DB 4; Length 1830121;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 TTTATTATTATGTTG 250
|||||
DB 466814 TTTATTATTATGTTG 466830

RESULT 39
US-08-290-937B-7/c
Sequence 7, Application US/08290937B
Patent No. 5648233
GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, KYOJI
APPLICANT: SHIMA, NOBUYUKI
APPLICANT: MURAKAMI, AKIHICO
APPLICANT: GOTO, MASAKI
APPLICANT: TSUDA, EISUKE
APPLICANT: MASUNAGA, HIROAKI
APPLICANT: TAKAHIRA, REIKO
APPLICANT: OOGAKI, FUMIKO
APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANUJI
TITLE OF INVENTION: MODIFIED TCF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tesla, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OLIGONUCLEOTIDE"
US-08-290-937B-7

Query Match 2.6%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTCTGATGATCCAG 17
|||||
DB 17 TGTCTGATGATCCAG 2

RESULT 40
US-08-552-369-3/c

Sequence 3, Application US/08552369
Patent No. 6241989
GENERAL INFORMATION:
APPLICANT: Scott, Fred W.
APPLICANT: Ngichabe, Christopher K.
APPLICANT: Hu, Liangbiao
TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/552,369
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/190,789
FILING DATE: 01/27/1994
APPLICATION NUMBER: 07/726,609
FILING DATE: 07/09/1991
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 18617.0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOHETICAL: no
FEATURE: P1 late promoter and leader sequence
US-08-552-369-3

Query Match 2.6%; Score 16; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTCTACTATATTTTA 190
|||||
DB 16 TTCTACTATATTTTA 1

Search completed: October 8, 2003, 07:53:20
Job time : 92 secs

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 07:19:17 ; Search time 190 Seconds
(without alignments)

8494.593 Million cell updates/sec

Title: US-10-010-160-1

Perfect score: 622

Sequence: 1 atgtcgtatgcacccagtaa.....aattatgcagtcgcagatc 622

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1731049 seqs, 1297405648 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	622	100.0	622	US-10-010-160-1	Sequence 1, Appl1
2	622	100.0	622	US-10-027-632-47579	Sequence 47579, A
3	622	100.0	622	US-10-027-632-75231	Sequence 75231, A
4	622	100.0	622	US-10-027-632-313525	Sequence 313525, A
5	622	100.0	622	US-10-060-036-1428	Sequence 1428, Ap
6	622	100.0	622	US-09-864-761-5935	Sequence 5935, Ap
7	622	100.0	622	US-10-027-632-220095	Sequence 220095, Ap
8	622	100.0	622	US-10-027-632-220096	Sequence 220096, Ap
9	622	100.0	622	US-10-027-632-220097	Sequence 220097, Ap
10	622	100.0	622	US-10-027-632-220098	Sequence 220098, Ap
11	622	100.0	622	US-10-027-632-220099	Sequence 220099, Ap
12	622	100.0	622	US-10-027-632-220100	Sequence 220100, Ap
13	622	100.0	622	US-10-313-542-28	Sequence 28, Appl1
14	622	100.0	622	US-09-887-527-53	Sequence 53, Appl1
15	622	100.0	622	US-09-764-891-8977	Sequence 8977, Ap
16	622	100.0	622	US-09-764-891-8978	Sequence 8978, Ap

17	3318	13	US-10-044-090-452	Sequence 452, App
18	10468	11	US-09-764-891-8976	Sequence 8976, Ap
19	10468	11	US-09-764-891-8979	Sequence 8979, Ap
20	42500	14	US-10-007-078-10	Sequence 10, Appl
21	161280	14	US-10-144-649A-746	Sequence 746, App
22	513509	11	US-09-754-853A-4	Sequence 4, Appl1
23	1503841	9	US-09-795-668-1	Sequence 1, Appl1
24	1503841	9	US-09-795-668-1	Sequence 1, Appl1
25	1503841	10	US-09-946-807-1	Sequence 1, Appl1
26	1561139	14	US-10-067-514-1	Sequence 1, Appl1
27	1386778	13	US-10-027-632-14961	Sequence 14961, Appl1
28	3309400	10	US-09-738-626-1	Sequence 1, Appl1
29	3309400	10	US-10-312-841-1	Sequence 1, Appl1
30	393	13	US-09-878-574-67	Sequence 67, Appl1
31	393	13	US-10-027-632-134481	Sequence 134481, Appl1
32	494	13	US-10-027-632-192884	Sequence 192884, Appl1
33	561	9	US-09-728-445-491	Sequence 491, App
34	561	9	US-09-864-761-14909	Sequence 14909, A
35	585	13	US-10-027-632-215080	Sequence 215080, Appl1
36	585	13	US-10-027-632-215081	Sequence 215081, Appl1
37	624	13	US-10-027-632-192200	Sequence 192200, Appl1
38	1114	13	US-10-027-632-117860	Sequence 117860, Appl1
39	1440	9	US-09-764-870-30	Sequence 30, Appl1
40	1440	14	US-10-125-540-30	Sequence 30, Appl1
41	2628	12	US-10-241-596-127	Sequence 127, App
42	2631	12	US-10-241-596-125	Sequence 125, App
43	2631	12	US-10-241-596-129	Sequence 129, App
44	2643	12	US-10-241-596-123	Sequence 123, App
45	2708	12	US-10-241-596-131	Sequence 131, App
46	2739	12	US-10-241-596-115	Sequence 115, App
47	2831	9	US-10-241-596-133	Sequence 133, App
48	3181	12	US-09-838-529-1	Sequence 1, Appl1
49	3281	14	US-10-198-846-12634	Sequence 12634, A
50	3647	12	US-10-241-596-134	Sequence 134, App
51	3876	13	US-10-051-952-4	Sequence 4, Appl1
52	4231	12	US-09-930-213-287	Sequence 287, App
53	4886	12	US-10-241-596-136	Sequence 136, App
54	5076	12	US-10-241-596-135	Sequence 135, App
55	5870	14	US-10-205-823-1	Sequence 1, Appl1
56	6082	9	US-09-759-143-535	Sequence 535, App
57	6082	9	US-09-780-669-535	Sequence 535, App
58	6082	9	US-09-822-827-535	Sequence 535, App
59	6082	10	US-09-895-793-535	Sequence 535, App
60	6082	10	US-09-895-814-535	Sequence 535, App
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63	6082	12	US-10-012-896-535	Sequence 535, App
64	6082	14	US-10-010-940-535	Sequence 535, App
65	8102	10	US-09-070-927A-244	Sequence 244, App
66	8108	12	US-10-200-562-77	Sequence 77, Appl1
67	8108	12	US-10-237-551-77	Sequence 77, Appl1
68	8108	14	US-10-121-988-77	Sequence 77, Appl1
69	8333	12	US-10-311-455-1475	Sequence 1475, App
70	8333	12	US-10-240-453-129	Sequence 129, App
71	8333	14	US-10-319-676-113	Sequence 113, App
72	17538	12	US-10-311-455-1130	Sequence 1130, App
73	51552	9	US-09-733-294A-30	Sequence 30, Appl1
74	640681	10	US-09-790-988-1	Sequence 1, Appl1
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76	3673778	12	US-10-312-841-2	Sequence 2, Appl1
77	226	9	US-09-874-138-7	Sequence 7, Appl1
78	226	13	US-10-005-842-7	Sequence 7, Appl1
79	307	10	US-09-783-590-637	Sequence 637, App
80	350	14	US-10-198-846-13101	Sequence 13101, A
81	455	13	US-10-027-632-201659	Sequence 201659, App
82	455	13	US-10-027-632-201660	Sequence 201660, App
83	474	11	US-09-918-995-23154	Sequence 23154, A
84	486	13	US-10-027-632-194989	Sequence 194989, App
85	486	13	US-10-027-632-194990	Sequence 194990, App
86	510	13	US-10-027-632-61864	Sequence 61864, A
87	510	13	US-10-027-632-61865	Sequence 61865, A
88	517	13	US-10-027-632-215995	Sequence 215995, App
89	524	13	US-10-027-632-35352	Sequence 35352, A

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C 93	17	2.7	528	12	US-09-814-353-7331	Sequence 7331, App	166	17	2.7	7573	10	US-09-880-107-2195	Sequence 2195, App
C 94	17	2.7	536	12	US-09-814-353-13716	Sequence 13716, A	167	17	2.7	7634	10	US-10-198-846-10420	Sequence 10420, A
C 95	17	2.7	538	13	US-10-027-632-274009	Sequence 274009, A	168	17	2.7	9130	14	US-10-311-455-2402	Sequence 2402, App
C 96	17	2.7	538	13	US-10-027-632-274010	Sequence 274010, A	C 169	17	2.7	12211	12	US-10-311-455-627	Sequence 627, App
C 97	17	2.7	538	13	US-10-027-632-274011	Sequence 274011, A	C 170	17	2.7	59446	12	US-09-820-449-3	Sequence 3, App
C 98	17	2.7	555	13	US-10-027-632-37208	Sequence 37208, A	C 171	17	2.7	90541	9	US-09-759-359A-3	Sequence 3, App
C 99	17	2.7	572	13	US-10-027-632-33049	Sequence 33049, A	C 172	17	2.7	90541	12	US-10-207-273-3	Sequence 3, App
C 100	17	2.7	586	13	US-10-027-632-191824	Sequence 191824, A	C 173	17	2.7	107820	12	US-09-792-616-1	Sequence 1, App
C 101	17	2.7	586	13	US-10-027-632-191825	Sequence 191825, A	C 174	17	2.7	123192	14	US-10-175-523-71	Sequence 71, App
C 102	17	2.7	611	13	US-10-027-632-224564	Sequence 224564, A	C 175	17	2.7	123908	14	US-10-270-875-1	Sequence 1, App
C 103	17	2.7	624	13	US-10-027-632-224841	Sequence 224841, A	C 176	17	2.7	123908	14	US-10-270-878-1	Sequence 1, App
C 104	17	2.7	632	13	US-10-027-632-191331	Sequence 191331, A	C 177	17	2.7	123908	14	US-10-270-786-1	Sequence 1, App
C 105	17	2.7	637	13	US-10-027-632-202228	Sequence 202228, A	C 178	17	2.7	123908	14	US-10-270-710-1	Sequence 1, App
C 106	17	2.7	652	13	US-10-027-632-277415	Sequence 277415, A	C 179	17	2.7	123908	14	US-10-270-859-1	Sequence 1, App
C 107	17	2.7	668	12	US-10-002-631C-255	Sequence 255, App	C 180	17	2.7	123908	15	US-10-270-846-1	Sequence 1, App
C 108	17	2.7	701	13	US-10-027-632-33553	Sequence 33553, A	C 181	17	2.7	159095	14	US-10-017-128-3	Sequence 3, App
C 109	17	2.7	726	13	US-10-027-632-255325	Sequence 255325, A	C 182	17	2.7	373361	11	US-09-901-136-3	Sequence 3, App
C 110	17	2.7	750	12	US-10-032-585-6495	Sequence 6495, App	C 183	17	2.7	659158	10	US-09-771-208-20	Sequence 20, App
C 111	17	2.7	831	13	US-10-027-632-10763	Sequence 10763, A	C 184	17	2.7	1631139	14	US-10-067-514-1	Sequence 1, App
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C 113	17	2.7	854	14	US-10-198-846-10645	Sequence 10645, A	C 186	17	2.7	3309400	10	US-09-738-626-1	Sequence 1, App
C 114	17	2.7	923	13	US-10-027-632-169506	Sequence 169506, A	C 187	17	2.7	9025608	14	US-10-156-761-1	Sequence 1, App
C 115	17	2.7	923	13	US-10-027-632-169507	Sequence 169507, A	C 188	17	2.7	9025608	14	US-10-156-761-1	Sequence 1, App
C 116	17	2.7	1044	13	US-10-027-632-117702	Sequence 117702, A	C 189	16	2.6	65	12	US-09-832-899-15	Sequence 15, App
C 117	17	2.7	1248	10	US-09-938-842A-298	Sequence 298, App	C 190	16	2.6	111	12	US-09-832-899-13	Sequence 13, App
C 118	17	2.7	1337	13	US-10-044-622-2	Sequence 2, App	C 191	16	2.6	140	9	US-09-864-761-30072	Sequence 30072, A
C 119	17	2.7	1351	13	US-10-027-632-358839	Sequence 358839, A	C 192	16	2.6	155	14	US-10-102-806-417	Sequence 417, App
C 120	17	2.7	1799	9	US-09-828-739-1	Sequence 1, App	C 193	16	2.6	173	10	US-09-783-590-3094	Sequence 3094, App
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C 127	17	2.7	1819	14	US-10-114-170-188	Sequence 188, App	C 200	16	2.6	285	10	US-10-083-357-91	Sequence 91, App
C 128	17	2.7	1864	13	US-10-139-876-3	Sequence 3, App	C 201	16	2.6	285	10	US-09-878-574-8266	Sequence 8266, App
C 129	17	2.7	1864	13	US-10-139-876-17	Sequence 17, App	C 202	16	2.6	292	10	US-09-867-701-6904	Sequence 6904, App
C 130	17	2.7	1864	13	US-10-139-876-19	Sequence 19, App	C 203	16	2.6	307	14	US-10-178-213-295	Sequence 295, App
C 131	17	2.7	2000	10	US-09-938-842A-4063	Sequence 4063, App	C 204	16	2.6	314	9	US-09-775-938A-23	Sequence 23, App
C 132	17	2.7	2004	10	US-09-887-576-223	Sequence 223, App	C 205	16	2.6	315	9	US-09-775-938A-9	Sequence 9, App
C 133	17	2.7	2029	10	US-09-956-095-1	Sequence 1, App	C 206	16	2.6	350	10	US-09-783-590-1609	Sequence 1609, App
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C 139	17	2.7	2029	14	US-10-161-694-4	Sequence 4, App	C 212	16	2.6	405	11	US-09-918-995-33569	Sequence 33569, A
C 140	17	2.7	2070	13	US-10-027-632-261195	Sequence 261195, A	C 213	16	2.6	410	10	US-09-983-965-4017	Sequence 4017, App
C 141	17	2.7	2888	13	US-10-027-632-111927	Sequence 111927, A	C 214	16	2.6	413	13	US-10-027-632-39626	Sequence 39626, A
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C 145	17	2.7	3964	9	US-09-757-421-3	Sequence 3, App	C 218	16	2.6	421	13	US-10-027-632-104573	Sequence 104573, A
C 146	17	2.7	3964	10	US-09-811-088-5	Sequence 5, App	C 219	16	2.6	425	13	US-10-027-632-296841	Sequence 296841, A
C 147	17	2.7	3964	14	US-10-314-410-5	Sequence 5, App	C 220	16	2.6	425	13	US-10-027-632-1606	Sequence 1606, App
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C 152	17	2.7	4053	14	US-10-037-270-156	Sequence 156, App	C 225	16	2.6	452	13	US-10-027-632-91250	Sequence 91250, A
C 153	17	2.7	4168	13	US-10-042-417-27	Sequence 27, App	C 226	16	2.6	452	13	US-10-027-632-91251	Sequence 91251, A
C 154	17	2.7	5040	12	US-10-311-455-2378	Sequence 2378, App	C 227	16	2.6	452	13	US-10-027-632-326056	Sequence 326056, A
C 155	17	2.7	5144	9	US-09-824-735-1	Sequence 1, App	C 228	16	2.6	452	13	US-10-027-632-317655	Sequence 317655, A
C 156	17	2.7	5396	12	US-10-240-485-153	Sequence 153, App	C 229	16	2.6	452	13	US-10-027-632-317657	Sequence 317657, A
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C 158	17	2.7	5929	12	US-10-311-455-682	Sequence 682, App	C 231	16	2.6	452	13	US-10-027-632-317659	Sequence 317659, A
C 159	17	2.7	5930	12	US-09-814-353-19600	Sequence 19600, App	C 232	16	2.6	456	13	US-10-027-632-11145	Sequence 11145, A
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C 162	17	2.7	6531	12	US-10-311-455-613	Sequence 613, App	C 235	16	2.6	457	10	US-09-897-778-306	Sequence 306, App

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C 237	16	2.6	457	12	US-10-117-982-306	Sequence 306, App	C 310	16	2.6	572	13	US-10-027-632-236789	Sequence 236789,
C 238	16	2.6	457	13	US-10-027-632-59016	Sequence 59016, A	C 311	16	2.6	572	13	US-10-027-632-236790	Sequence 236790,
C 239	16	2.6	459	13	US-10-027-632-183056	Sequence 183056, A	C 312	16	2.6	575	13	US-10-027-632-236791	Sequence 236791,
C 240	16	2.6	459	13	US-10-027-632-183057	Sequence 183057, A	C 313	16	2.6	575	13	US-10-027-632-78488	Sequence 78488, A
C 241	16	2.6	467	13	US-10-027-632-43394	Sequence 43394, A	C 314	16	2.6	575	13	US-10-027-632-78489	Sequence 78489, A
C 242	16	2.6	467	13	US-10-027-632-43395	Sequence 43395, A	C 315	16	2.6	575	13	US-10-027-632-78975	Sequence 78975, A
C 243	16	2.6	470	9	US-09-864-761-1460	Sequence 1460, App	C 316	16	2.6	575	13	US-10-027-632-78976	Sequence 78976, A
C 244	16	2.6	471	11	US-09-918-995-21289	Sequence 21289, A	C 317	16	2.6	575	13	US-10-027-632-300824	Sequence 300824,
C 245	16	2.6	474	11	US-09-918-995-22891	Sequence 22891, A	C 318	16	2.6	577	13	US-10-027-632-300825	Sequence 300825,
C 246	16	2.6	481	13	US-10-027-632-275760	Sequence 275760, A	C 319	16	2.6	577	13	US-10-027-632-248564	Sequence 248564,
C 247	16	2.6	482	13	US-09-917-800A-581	Sequence 581, App	C 320	16	2.6	577	13	US-10-027-632-248565	Sequence 248565,
C 248	16	2.6	482	11	US-09-918-995-16005	Sequence 16005, A	C 321	16	2.6	578	9	US-09-864-761-9937	Sequence 9937, App
C 249	16	2.6	488	9	US-09-864-761-11641	Sequence 11641, A	C 322	16	2.6	583	9	US-09-864-761-13527	Sequence 13527, A
C 250	16	2.6	490	13	US-10-027-632-185355	Sequence 185355, A	C 323	16	2.6	583	13	US-10-027-632-205656	Sequence 205656,
C 251	16	2.6	491	13	US-10-027-632-6415	Sequence 6415, App	C 324	16	2.6	585	13	US-10-027-632-205657	Sequence 205657,
C 252	16	2.6	491	13	US-10-027-632-6416	Sequence 6416, App	C 325	16	2.6	585	13	US-10-027-632-223078	Sequence 223078,
C 253	16	2.6	491	13	US-10-027-632-324635	Sequence 324635, App	C 326	16	2.6	590	13	US-10-027-632-213503	Sequence 213503,
C 254	16	2.6	493	10	US-09-070-927A-822	Sequence 822, App	C 327	16	2.6	591	13	US-10-027-632-255294	Sequence 255294,
C 255	16	2.6	493	13	US-10-027-632-274838	Sequence 274838, App	C 328	16	2.6	591	13	US-10-027-632-255295	Sequence 255295,
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C 257	16	2.6	503	12	US-09-921-406C-30	Sequence 30, App	C 330	16	2.6	596	13	US-10-027-632-296831	Sequence 296831,
C 258	16	2.6	505	11	US-09-746-783-17	Sequence 17, App	C 331	16	2.6	598	9	US-09-864-761-6378	Sequence 6378, App
C 259	16	2.6	506	10	US-09-783-590-5680	Sequence 5680, App	C 332	16	2.6	598	13	US-10-027-632-218791	Sequence 218791,
C 260	16	2.6	518	13	US-10-027-632-126177	Sequence 126177, A	C 333	16	2.6	598	13	US-10-027-632-218792	Sequence 218792,
C 261	16	2.6	519	13	US-10-027-632-41720	Sequence 41720, A	C 334	16	2.6	599	13	US-10-027-632-103	Sequence 103, App
C 262	16	2.6	520	13	US-10-027-632-208269	Sequence 208269, A	C 335	16	2.6	599	13	US-10-027-632-104	Sequence 104, App
C 263	16	2.6	520	13	US-10-027-632-208270	Sequence 208270, A	C 336	16	2.6	599	13	US-10-027-632-105	Sequence 105, App
C 264	16	2.6	525	10	US-09-974-300-5987	Sequence 5987, App	C 337	16	2.6	599	13	US-10-027-632-60264	Sequence 60264, A
C 265	16	2.6	530	13	US-10-027-632-65517	Sequence 65517, A	C 338	16	2.6	601	13	US-10-027-632-262132	Sequence 262132,
C 266	16	2.6	530	13	US-10-027-632-296405	Sequence 296405, A	C 339	16	2.6	601	13	US-10-027-632-262133	Sequence 262133,
C 267	16	2.6	533	13	US-10-027-632-240455	Sequence 240455, A	C 340	16	2.6	602	13	US-10-027-632-205823	Sequence 205823,
C 268	16	2.6	535	13	US-10-027-632-206990	Sequence 206990, A	C 341	16	2.6	604	11	US-09-791-279-103	Sequence 103, App
C 269	16	2.6	539	13	US-10-027-632-281638	Sequence 281638, A	C 342	16	2.6	604	13	US-10-027-632-54421	Sequence 54421, A
C 270	16	2.6	539	13	US-10-027-632-281639	Sequence 281639, A	C 343	16	2.6	604	13	US-10-027-632-54422	Sequence 54422, A
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C 272	16	2.6	542	13	US-10-027-632-50578	Sequence 50578, A	C 345	16	2.6	604	13	US-10-027-632-301577	Sequence 301577,
C 273	16	2.6	542	13	US-10-027-632-306621	Sequence 306621, A	C 346	16	2.6	604	13	US-10-027-632-301578	Sequence 301578,
C 274	16	2.6	542	13	US-10-027-632-306622	Sequence 306622, A	C 347	16	2.6	604	13	US-10-027-632-301579	Sequence 301579,
C 275	16	2.6	543	13	US-10-027-632-264798	Sequence 264798, A	C 348	16	2.6	608	13	US-10-027-632-216069	Sequence 216069,
C 276	16	2.6	543	13	US-10-027-632-264799	Sequence 264799, A	C 349	16	2.6	611	13	US-10-027-632-202649	Sequence 202649,
C 277	16	2.6	546	13	US-10-027-632-307649	Sequence 307649, A	C 350	16	2.6	611	13	US-10-027-632-208484	Sequence 208484,
C 278	16	2.6	546	13	US-10-027-632-321406	Sequence 321406, A	C 351	16	2.6	614	13	US-10-027-632-99733	Sequence 99733, A
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C 280	16	2.6	548	13	US-10-027-632-82344	Sequence 82344, A	C 353	16	2.6	615	12	US-09-814-353-9889	Sequence 9889, App
C 281	16	2.6	548	13	US-10-027-632-83251	Sequence 83251, A	C 354	16	2.6	615	13	US-10-051-902-17	Sequence 17, App
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C 284	16	2.6	549	13	US-10-027-632-51136	Sequence 51136, A	C 357	16	2.6	615	13	US-10-027-632-255157	Sequence 255157,
C 285	16	2.6	555	13	US-10-027-632-222300	Sequence 222300, A	C 358	16	2.6	620	12	US-09-814-353-16273	Sequence 16273, A
C 286	16	2.6	555	13	US-10-027-632-222300	Sequence 222300, A	C 359	16	2.6	622	13	US-10-027-632-272937	Sequence 272937,
C 287	16	2.6	559	13	US-10-027-632-219347	Sequence 219347, A	C 360	16	2.6	622	13	US-10-027-632-272938	Sequence 272938,
C 288	16	2.6	559	13	US-10-027-632-219348	Sequence 219348, A	C 361	16	2.6	623	13	US-10-027-632-276707	Sequence 276707,
C 289	16	2.6	560	13	US-10-027-632-269688	Sequence 269688, A	C 362	16	2.6	624	13	US-10-027-632-191999	Sequence 191999,
C 290	16	2.6	562	13	US-10-027-632-270485	Sequence 270485, A	C 363	16	2.6	624	13	US-10-027-632-191999	Sequence 191999,
C 291	16	2.6	564	13	US-10-027-632-90533	Sequence 90533, A	C 364	16	2.6	626	13	US-10-027-632-217688	Sequence 217688,
C 292	16	2.6	564	13	US-10-027-632-90534	Sequence 90534, A	C 365	16	2.6	626	13	US-10-027-632-129060	Sequence 129060,
C 293	16	2.6	565	13	US-10-027-632-38861	Sequence 38861, A	C 366	16	2.6	632	13	US-10-027-632-196658	Sequence 196658,
C 294	16	2.6	565	13	US-10-027-632-38862	Sequence 38862, A	C 367	16	2.6	633	13	US-10-027-632-196659	Sequence 196659,
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C 297	16	2.6	566	13	US-10-027-632-295663	Sequence 295663, A	C 370	16	2.6	637	13	US-10-027-632-231492	Sequence 231492,
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C 299	16	2.6	567	13	US-10-027-632-65674	Sequence 65674, A	C 372	16	2.6	644	13	US-10-027-632-116150	Sequence 116150,
C 300	16	2.6	567	13	US-10-027-632-65675	Sequence 65675, A	C 373	16	2.6	646	13	US-10-027-632-206528	Sequence 206528,
C 301	16	2.6	567	13	US-10-027-632-198285	Sequence 198285, A	C 374	16	2.6	649	13	US-10-027-632-46290	Sequence 46290, A
C 302	16	2.6	567	13	US-10-027-632-198286	Sequence 198286, A	C 375	16	2.6	649	13	US-10-027-632-46291	Sequence 46291, A
C 303	16	2.6	567	13	US-10-027-632-295865	Sequence 295865, A	C 376	16	2.6	649	13	US-10-027-632-228874	Sequence 228874,
C 304	16	2.6	567	13	US-10-027-632-295866	Sequence 295866, A	C 377	16	2.6	650	13	US-10-027-632-214107	Sequence 214107,
C 305	16	2.6	568	9	US-09-864-761-9029	Sequence 9029, App	C 378	16	2.6	650	13	US-10-027-632-214107	Sequence 214107,
C 306	16	2.6	569	13	US-10-027-632-270693	Sequence 270693, App	C 379	16	2.6	655	13	US-10-027-632-206121	Sequence 206121,
C 307	16	2.6	571	13	US-10-027-632-254618	Sequence 254618, App	C 380	16	2.6	656	11	US-09-764-891-8741	Sequence 8741, App
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C 335	16	2.6	663	13	US-10-027-632-79910	Sequence 79910, A
C 336	16	2.6	663	13	US-10-027-632-182689	Sequence 182689,
C 337	16	2.6	663	13	US-10-027-632-182690	Sequence 182690,
C 338	16	2.6	664	13	US-10-027-632-278561	Sequence 278561,
C 339	16	2.6	664	13	US-10-027-632-278583	Sequence 275833,
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C 343	16	2.6	708	13	US-10-027-632-280732	Sequence 25780, A
C 344	16	2.6	709	13	US-10-027-632-25780	Sequence 249390,
C 345	16	2.6	720	13	US-10-027-632-21419	Sequence 21419, A
C 346	16	2.6	726	13	US-10-027-632-173428	Sequence 113428,
C 347	16	2.6	729	13	US-10-027-632-14417	Sequence 14417, A
C 348	16	2.6	729	13	US-10-027-632-37279	Sequence 27279, A
C 349	16	2.6	731	13	US-10-027-632-37279	Sequence 33775, A
C 350	16	2.6	731	13	US-10-027-632-33776	Sequence 33776, A
C 351	16	2.6	731	13	US-10-027-632-33776	Sequence 33777, A
C 352	16	2.6	732	13	US-10-027-632-385196	Sequence 285196,
C 353	16	2.6	732	13	US-10-027-632-385197	Sequence 285197,
C 354	16	2.6	732	13	US-10-027-632-285198	Sequence 285198,
C 355	16	2.6	733	13	US-10-027-632-11575	Sequence 11575, A
C 356	16	2.6	736	9	US-09-775-938A-11	Sequence 11, Appl
C 357	16	2.6	740	13	US-10-027-632-126357	Sequence 126357,
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C 360	16	2.6	778	14	US-10-175-523-15	Sequence 15, Appl
C 361	16	2.6	780	13	US-10-027-632-29003	Sequence 29003, A
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C 364	16	2.6	803	13	US-10-027-632-174228	Sequence 174228,
C 365	16	2.6	811	13	US-10-027-632-167050	Sequence 167050,
C 366	16	2.6	818	13	US-10-027-632-169140	Sequence 169140,
C 367	16	2.6	820	13	US-10-027-632-169141	Sequence 169141,
C 368	16	2.6	820	13	US-10-027-632-162212	Sequence 162212,
C 369	16	2.6	823	13	US-10-027-632-142858	Sequence 142858,
C 370	16	2.6	824	13	US-10-027-632-140112	Sequence 140112,
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C 375	16	2.6	839	13	US-10-027-632-168087	Sequence 168087,
C 376	16	2.6	847	13	US-10-027-632-168662	Sequence 168662,
C 377	16	2.6	873	14	US-10-283-769-7	Sequence 7, Appl
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C 379	16	2.6	887	13	US-10-027-632-50550	Sequence 50550, A
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C 381	16	2.6	929	9	US-09-452-239-19	Sequence 19, Appl
C 382	16	2.6	962	9	US-09-452-239-23	Sequence 23, Appl
C 383	16	2.6	965	13	US-10-027-632-10084	Sequence 120084,
C 384	16	2.6	980	9	US-09-452-239-21	Sequence 21, Appl
C 385	16	2.6	1010	13	US-10-027-632-119331	Sequence 119331,
C 386	16	2.6	1010	13	US-10-027-632-122301	Sequence 122301,
C 387	16	2.6	1023	9	US-09-452-239-25	Sequence 25, Appl
C 388	16	2.6	1026	16	US-10-102-806-168	Sequence 168,
C 389	16	2.6	1034	13	US-10-027-632-250680	Sequence 250680,
C 390	16	2.6	1034	13	US-10-027-632-250681	Sequence 250681,
C 391	16	2.6	1067	13	US-10-027-632-249826	Sequence 249826,
C 392	16	2.6	1099	12	US-10-017-161-2253	Sequence 2253, Ap
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C 395	16	2.6	1100	13	US-10-027-632-119652	Sequence 119652,
C 396	16	2.6	1100	13	US-10-027-632-118236	Sequence 118236,
C 397	16	2.6	1161	13	US-10-027-632-118237	Sequence 118237,
C 398	16	2.6	1161	13	US-10-027-632-118237	Sequence 118237,
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C 401	16	2.6	1169	13	US-10-027-632-118872	Sequence 118872,
C 402	16	2.6	1169	13	US-10-027-632-118873	Sequence 118873,
C 403	16	2.6	1178	13	US-10-027-632-251821	Sequence 251821,
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C 405	16	2.6	1225	13	US-10-027-632-265685	Sequence 265685,
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684	16	2.6	74862	14	US-10-274-974-3	Sequence 3, Appli	757	15	2.4	315	10	US-09-963-965-2450	Sequence 2450, Ap
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690	16	2.6	162025	12	US-10-272-665-36	Sequence 36, Appl	763	15	2.4	321	10	US-09-849-626-1500	Sequence 1500, Ap
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696	16	2.6	202001	14	US-10-274-990-3	Sequence 3, Appli	769	15	2.4	328	14	US-10-092-154-267	Sequence 267, App
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702	16	2.6	392000	12	US-10-027-983-11	Sequence 11, Appl	775	15	2.4	350	11	US-09-921-936-98	Sequence 98, Appl
703	16	2.6	465237	10	US-09-933-267A-4	Sequence 4, Appli	776	15	2.4	354	10	US-09-962-832-97	Sequence 77, Appl
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707	16	2.6	786431	12	US-10-412-277-3	Sequence 3, Appli	780	15	2.4	358	11	US-09-991-936-569	Sequence 569, App
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ALIGNMENTS

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; APPLICANT: Rosey, Everett L.
; APPLICANT: Strugnell, Richard A.
; APPLICANT: Good, Robert T.
; APPLICANT: King, Kendall W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
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; CURRENT APPLICATION NUMBER: US/10/010,160
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QY 1 ATGCTGATGATCCCAAGAAAACAGAAACCAACCCGAAACGACGTCAGAGCTCGT 60
DB 1 ATGCTGATGATCCCAAGAAAACAGAAACCAACCCGAAACGACGTCAGAGCTCGT 60
QY 61 TCTGAAGGAGTGTCCCTAAATCAGAGAGTTTCTAAGATTTGACTCTGACGAGGG 120
DB 61 TCTGAAGGAGTGTCCCTAAATCAGAGAGTTTCTAAGATTTGACTCTGACGAGGG 120
QY 121 ATGCGGGGCTGTCTATTATTTAGCGGTAATGGAAGTCACTTTGAAACAATTTTCTAC 180
DB 121 ATGCGGGGCTGTCTATTATTTAGCGGTAATGGAAGTCACTTTGAAACAATTTTCTAC 180
QY 181 TATATTTTTCAGAAATCATTTGCTTTAGGTTACAGACAGTCAGATATGCTTTATTT 240
DB 181 TATATTTTTCAGAAATCATTTGCTTTAGGTTACAGACAGTCAGATATGCTTTATTT 240
QY 241 ATTATATGTTGTCAGAGATATGCTTTATTTATGATATGCAATATATCTTTATGCTGT 300
DB 241 ATTATATGTTGTCAGAGATATGCTTTATTTATGATATGCAATATATCTTTATGCTGT 300
QY 301 ACGGATGATTTTCATTACGTCATGATGATGTCATTTATGATGATGATGATTTTAAA 360
DB 301 ACGGATGATTTTCATTACGTCATGATGATGTCATTTATGATGATGATGATTTTAAA 360
QY 361 TTTAAATGAGTAAATTTATATATATATATATATATATATATATATATATATATAT 420
DB 361 TTTAAATGAGTAAATTTATATATATATATATATATATATATATATATATATATAT 420
QY 421 ACATGTTGCACTTTTACGATGTTTGTCAATATGTTATATGATATGTTCCATAT 480
DB 421 ACATGTTGCACTTTTACGATGTTTGTCAATATGTTATATGATATGTTCCATAT 480
QY 481 ATGATTTAAAGAGAGATTTTCAAACTTTTACCATATATATATATATATATATAT 540
DB 481 ATGATTTAAAGAGAGATTTTCAAACTTTTACCATATATATATATATATATATAT 540
QY 541 GTGGCAGATTATATGCTTAATATACAGAAATGACTGTTTATATATAGCTTAATG 600
DB 541 GTGGCAGATTATATGCTTAATATACAGAAATGACTGTTTATATATAGCTTAATG 600
QY 601 ACAATTTATGACGCGGAGATC 622
DB 601 ACAATTTATGACGCGGAGATC 622

```

```

RESULT 2
US-10-027-632-47579
; Sequence 47579, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/219,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47579
; LENGTH: 622

```

TYPE: DNA
ORGANISM: Human
US-10-027-632-47579

Query Match
Best Local Similarity 3.2%; Score 20; DB 13; Length 622;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 GTTTTAAATTAAATGAG 371
|||||
Db 317 GTTTTAAATTAAATGAG 336

RESULT 3
US-10-027-632-75231
Sequence 75231, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75231
LENGTH: 624
TYPE: DNA
ORGANISM: Human
US-10-027-632-75231

Query Match
Best Local Similarity 3.2%; Score 20; DB 13; Length 624;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 GTTTTAAATTAAATGAG 371
|||||
Db 319 GTTTTAAATTAAATGAG 338

RESULT 4
US-10-027-632-313525
Sequence 313525, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 313525
LENGTH: 624
TYPE: DNA
ORGANISM: Human
US-10-027-632-313525

Query Match
Best Local Similarity 3.2%; Score 20; DB 13; Length 624;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 352 GTTTTAAATTAAATGAG 371
|||||
Db 319 GTTTTAAATTAAATGAG 338

RESULT 5
US-10-060-036-1428/c
Sequence 1428, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yugu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1428
LENGTH: 340
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 308
OTHER INFORMATION: n = A,T,C or G
US-10-060-036-1428

Query Match
Best Local Similarity 3.1%; Score 19; DB 14; Length 340;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 261 AGCTATTATTATGATGCCA 279
|||||
Db 307 AGCTATTATTATGATGCCA 289

RESULT 6
US-09-864-761-5935/c
Sequence 5935, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

```

; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5935
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004896.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
US-09-864-761-5935

Query Match      3.1%; Score 19; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      228 ATATGCTTTATTTATTTAT 246
Db      79 ATATGCTTTATTTATTTAT 61

RESULT 7
US-10-027-632-220095
; Sequence 220095, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT FILING DATE: 2002-04-30
```

```

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220096
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220096

Query Match      3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      183 TATTTTACAGATCATTT 201
Db      605 TATTTTACAGATCATTT 623

RESULT 8
US-10-027-632-220096
; Sequence 220096, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220096
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220096

Query Match      3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      183 TATTTTACAGATCATTT 201
Db      605 TATTTTACAGATCATTT 623

RESULT 9
```

```
US-10-027-632-220097
; Sequence 220097, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220097
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220097
```

```
Query Match          3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      183 TATTTTACAGATCATTT 201
        |||
Db      605 TATTTTACAGATCATTT 623
```

```
RESULT 10
US-10-027-632-220098
; Sequence 220098, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220098
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220098
```

```
Query Match          3.1%; Score 19; DB 13; Length 636;
```

```
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      183 TATTTTACAGATCATTT 201
        |||
Db      605 TATTTTACAGATCATTT 623
```

```
RESULT 11
US-10-027-632-220099
; Sequence 220099, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220099
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-220099
```

```
Query Match          3.1%; Score 19; DB 13; Length 636;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      183 TATTTTACAGATCATTT 201
        |||
Db      605 TATTTTACAGATCATTT 623
```

```
RESULT 12
US-10-027-632-220100
; Sequence 220100, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```


NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 220100
LENGTH: 636
TYPE: DNA
ORGANISM: Human
US-10-027-632-220100

Query Match
Best Local Similarity 100.0%; Score 19; DB 13; Length 636;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TATTTTACGAATCATTT 201
|||||
Db 605 TATTTTACGAATCATTT 623

RESULT 13
US-10-313-542-28
Sequence 28, Application US/10313542
Publication No. US20030120057A1
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED F
FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: US/10/313,542
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: US/09/495,050
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 28
LENGTH: 948
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20030120057A1 647628CT1
US-10-313-542-28

Query Match
Best Local Similarity 100.0%; Score 19; DB 14; Length 948;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 AGCTATTTTATGATGCCA 279
|||||
Db 678 AGCTATTTTATGATGCCA 696

RESULT 14
US-09-887-527-53/c
Sequence 53, Application US/09887527
Publication No. US20030055006A1
GENERAL INFORMATION:
APPLICANT: SIEMEISTER, GERRARD
APPLICANT: HABEREY, MARTIN
APPLICANT: THIERRAUCH, KARL-HEINZ
TITLE OF INVENTION: COMBINATIONS AND COMPOSITIONS WHICH INTERFERE WITH
TITLE OF INVENTION: VEGF/VEGF AND ANGIOPOITIN/TIE RECEPTOR FUNCTION
TITLE OF INVENTION: AND THEIR USE
FILE REFERENCE: SCH-1815
CURRENT APPLICATION NUMBER: US/09/887,527
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: DE 00250194.8
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: DE 00250214.4
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 53
LENGTH: 989
TYPE: DNA
ORGANISM: Homo sapiens
US-09-887-527-53

Query Match
Best Local Similarity 100.0%; Score 19; DB 11; Length 989;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
|||||
Db 771 ATTACTTTTATGCTGTT 753

RESULT 15
US-09-764-891-8977
Sequence 8977, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8977
LENGTH: 2422
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-8977

Query Match
Best Local Similarity 100.0%; Score 19; DB 11; Length 2422;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
|||||
Db 1593 ATTACTTTTATGCTGTT 1611

RESULT 16
US-09-764-891-8978
Sequence 8978, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8978
LENGTH: 2422
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-8978

Query Match
Best Local Similarity 100.0%; Score 19; DB 11; Length 2422;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 ATTACTTTTATGCTGTT 300
|||||
Db 1593 ATTACTTTTATGCTGTT 1611

RESULT 17
US-10-044-090-452

Sequence 452, Application US/10044090
Publication No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 452
LENGTH: 3318
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 199489.1
NAME/KEY: unsure
LOCATION: 1255, 1299
OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-452

Query Match 3.1%; Score 19; DB 13; Length 3318;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 261 AGCTATTATTGATGCCA 279
|||
Db 1507 AGCTATTATTGATGCCA 1525

RESULT 18
US-09-764-891-8976
Sequence 8976, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8976
LENGTH: 10468
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-8976

Query Match 3.1%; Score 19; DB 11; Length 10468;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 282 ATTACTTTTATGCTGTT 300
|||
Db 7435 ATTACTTTTATGCTGTT 7453

RESULT 19
US-09-764-891-8979
Sequence 8979, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8979

LENGTH: 10468
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-8979

Query Match 3.1%; Score 19; DB 11; Length 10468;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 282 ATTACTTTTATGCTGTT 300
|||
Db 7435 ATTACTTTTATGCTGTT 7453

RESULT 20
US-10-007-078-10
Sequence 10, Application US/10007078
Publication No. US20030105042A1
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF EIP2C1 EXPRESSION
FILE REFERENCE: RTS-0236
CURRENT APPLICATION NUMBER: US/10/007,078
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 42500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 18344-18443, 25149-25248, 27228-27327, 27357
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: intron
LOCATION: (820)...(5800)
OTHER INFORMATION: Intron 1
NAME/KEY: intron
LOCATION: (5985)...(9929)
OTHER INFORMATION: Intron 2
NAME/KEY: intron
LOCATION: (10051)...(10469)
OTHER INFORMATION: Intron 3
NAME/KEY: intron
LOCATION: (10652)...(11046)
OTHER INFORMATION: Intron 4
NAME/KEY: intron
LOCATION: (11184)...(11409)
OTHER INFORMATION: Intron 5
NAME/KEY: intron
LOCATION: (11545)...(11687)
OTHER INFORMATION: Intron 6
NAME/KEY: intron
LOCATION: (11776)...(12494)
OTHER INFORMATION: Intron 7
NAME/KEY: intron
LOCATION: (12643)...(18653)
OTHER INFORMATION: Intron 8
NAME/KEY: intron
LOCATION: (18774)...(19127)
OTHER INFORMATION: Intron 9
NAME/KEY: intron
LOCATION: (19251)...(19383)
OTHER INFORMATION: Intron 10
NAME/KEY: intron
LOCATION: (19518)...(24114)
OTHER INFORMATION: Intron 11
NAME/KEY: intron
LOCATION: (24300)...(30976)
OTHER INFORMATION: Intron 12
NAME/KEY: intron
LOCATION: (31137)...(31318)
OTHER INFORMATION: Intron 13

```
NAME/KEY: Intron
LOCATION: (31410)...(32482)
OTHER INFORMATION: Intron 14
NAME/KEY: Intron
LOCATION: (32678)...(34727)
OTHER INFORMATION: Intron 15
NAME/KEY: Intron
LOCATION: (34863)...(35456)
OTHER INFORMATION: Intron 16
NAME/KEY: Intron
LOCATION: (35559)...(36189)
OTHER INFORMATION: Intron 17
NAME/KEY: Intron
LOCATION: (36390)...(36633)
OTHER INFORMATION: Intron 18
NAME/KEY: Intron
LOCATION: (41435)...(42500)
OTHER INFORMATION: Intron 19
US-10-007-078-10
```

```
Query Match      3.1% Score 19; DB 14; Length 42500;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      352 GTTTTAAATTAAATGGA 370
DB      23190 GTTTTAAATTAAATGGA 23208
```

```
RESULT 21
US-10-144-649A-746/c
Sequence 746, Application US/10144649A
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 746
LENGTH: 161280
TYPE: DNA
ORGANISM: Homo sapiens
US-10-144-649A-746
```

```
Query Match      3.1% Score 19; DB 14; Length 161280;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      230 ATGCTTATTATTATATG 248
DB      113647 ATGCTTATTATTATATG 113629
```

```
RESULT 22
US-09-754-853A-4
Sequence 4, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with
FILE REFERENCE: 38-10(15810)B
```

```
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 4
LENGTH: 513509
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (11805)..(113968), (114684)..(115204)
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
```

```
Query Match      3.1% Score 19; DB 11; Length 513509;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      352 GTTTTAAATTAAATGGA 370
DB      425451 GTTTTAAATTAAATGGA 425469
```

```
RESULT 23
US-09-795-668-1/c
Sequence 1, Application US/09795668
Patent No. US2002004577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Guicher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)..(1531)
OTHER INFORMATION: d=a or g or t/u
```

```
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1
```

```
Query Match 3.1%; Score 19; DB 9; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 228 ATATGCTTTATTTATTTAT 246
Db 963911 ATATGCTTTATTTATTTAT 963893
```

RESULT 24

```
US-09-795-686-1/c
Sequence 1, Application US/09795686
Patent No. US20020094954A1
```

```
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinhorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
```

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: x=g or a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=c/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
```

```
OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1
```

```
Query Match 3.1%; Score 19; DB 9; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 228 ATATGCTTTATTTATTTAT 246
Db 963911 ATATGCTTTATTTATTTAT 963893
```

RESULT 25

```
US-09-946-807-1/c
Sequence 1, Application US/09946807
Patent No. US20020165144A1
```

```
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinhorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
```

```
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: x=g or a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=c/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
```

```
OTHER INFORMATION: v=a or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1
```

```
Query Match          3.1%: Score 19; DB 10; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      228 ATATGCTTATTTATTTAT 246
      |||||||
DB      963911 AATGCTTATTTATTTAT 963893
```

```
RESULT 26
US-10-067-514-1
; Sequence 1, Application US/10067514
; Publication No. US20030054531A1
```

```
GENERAL INFORMATION:
APPLICANT: Gtelardotcltr, Solveig
APPLICANT: Jonsdotcltr, Sif
APPLICANT: Reynisdotcltr, Sigridur Th.
TITLE OF INVENTION: HUMAN STROKE GENE
FILE REFERENCE: 2345.2010-003
CURRENT APPLICATION NUMBER: US/10/067,514
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 09/811/352
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1691139
TYPE: DNA
ORGANISM: Human
US-10-067-514-1
```

```
Query Match          3.1%: Score 19; DB 14; Length 1691139;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      169 ACAATTTCTACTATATTT 187
      |||||||
DB      681945 ACAATTTCTACTATATTT 681963
```

```
RESULT 27
US-10-027-632-174961/c
; Sequence 174961, Application US/10027632
; GENERAL INFORMATION:
```

```
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 174961
LENGTH: 3186778
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(3186778)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961
```

```
Query Match          3.1%: Score 19; DB 13; Length 3186778;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      360 ATTTAATGAGTAAATTT 378
      |||||||
DB      57048 ATTTAATGAGTAAATTT 57030
```

```
RESULT 28
US-09-738-626-1
```

```
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
```

```
Query Match          3.1%: Score 19; DB 10; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      376 TTTAATATATTAAGGCT 394
      |||||||
DB      1835974 TTTAATATATTAAGGCT 1835992
```

```
RESULT 29
US-10-312-841-1/c
```

```
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
```

LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (3294164)
US-10-312-841-1

Query Match 3.1%; Score 19; DB 12; Length 3673778;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 TAAATTATATATATAA 390
Db 2991275 TAAATTATATATATAA 2991257

RESULT 30
US-09-878-574-67

Sequence 67, Application US/09878574
Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 67

LENGTH: 393

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(393)

OTHER INFORMATION: unsure at all n locations

US-09-878-574-67

Query Match 2.9%; Score 18; DB 10; Length 393;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 353 TTTTAAATTTAAATGGA 370
Db 109 TTTTAAATTTAAATGGA 126

RESULT 31
US-10-027-632-134481

Sequence 134481, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 134481
LENGTH: 399
TYPE: DNA
ORGANISM: Human
US-10-027-632-134481

Query Match 2.9%; Score 18; DB 13; Length 399;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 GCAGCAGGATGCTGGG 129
Db 317 GCAGCAGGATGCTGGG 334

RESULT 32
US-10-027-632-192884

Sequence 192884, Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 192884

LENGTH: 494

TYPE: DNA

ORGANISM: Human

US-10-027-632-192884

Query Match 2.9%; Score 18; DB 13; Length 494;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 TTTTCTACTATATTTTA 190
Db 198 TTTTCTACTATATTTTA 215

RESULT 33
US-09-728-445-491

Sequence 491, Application US/09728445

Patent No. US20020102543A1

GENERAL INFORMATION:

APPLICANT: Friedrich, Glenn

APPLICANT: Zamdrowicz, Brian

APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020102543A1 Mutated Mammalian Cells and

FILE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,358
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 491
LENGTH: 546
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(546)
OTHER INFORMATION: n = A,T,C or G
US-09-728-445-491

Query Match 2.9%; Score 18; DB 10; Length 546;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 GCTATTATTGATGCCA 279
Db 114 GCTATTATTGATGCCA 131

RESULT 34
US-09-864-761-14909/C
Sequence 14909, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 14909
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009290.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
NAME/KEY: unsure
LOCATION: 95
NAME/KEY: unsure
LOCATION: 413
NAME/KEY: unsure
LOCATION: 414
NAME/KEY: unsure
LOCATION: 428
NAME/KEY: unsure
LOCATION: 434
NAME/KEY: unsure
LOCATION: 443
NAME/KEY: unsure
LOCATION: 465
US-09-864-761-14909

Query Match 2.9%; Score 18; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 159 TCATTGAAACAAATTT 176
Db 502 TCATTGAAACAAATTT 485

RESULT 35
US-10-027-632-215080
Sequence 215080, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 215080
LENGTH: 585
TYPE: DNA
ORGANISM: Human
US-10-027-632-215080

Query Match 2.9%; Score 18; DB 13; Length 585;
Best Local Similarity 100.0%; Pred. No. 97;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 ATATGCTTTATTATTTA 245
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Db 517 ATATGCTTTATTATTTA 534

RESULT 36
US-10-027-632-215081
; Sequence 215081, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215081
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-215081

Query Match 2.9%; Score 18; DB 13; Length 585;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 ATATGCTTTATTATTTA 245
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Db 517 ATATGCTTTATTATTTA 534

RESULT 37
US-10-027-632-192200/c
; Sequence 192200, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192200
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-192200

Query Match 2.9%; Score 18; DB 13; Length 624;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AAATTTAAATGAGATAA 375
|||||
Db 499 AAATTTAAATGAGATAA 482

RESULT 38
US-10-027-632-117860
; Sequence 117860, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117860
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-117860

Query Match 2.9%; Score 18; DB 13; Length 1114;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 TTACTTTTATTTGCTGTT 300
|||||
Db 377 TTACTTTTATTTGCTGTT 394

RESULT 39
US-09-764-870-30
; Sequence 30, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1440
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-764-870-30

Query Match 2.9%; Score 18; DB 9; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 AGGTTTTTAATTAAAT 367
|||||
Db 1335 AGGTTTTTAATTAAAT 1352

RESULT 40
US-10-125-540-30
; Sequence 30, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-540-30

Query Match 2.9%; Score 18; DB 14; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 AGGTTTTTAATTAAAT 367
|||||
Db 1335 AGGTTTTTAATTAAAT 1352

Search completed: October 8, 2003, 08:54:10
Job time : 242 secs

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2003, 06:22:36 ; Search time 1943 Seconds
(without alignments)
7780.434 Million cell updates/sec

Title: US-10-010-160-1
Perfect score: 622
Sequence: 1 atgtcgtatgatccagctaa.....aattatcgcagtcgacatc 622

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	21	3.4	461	10	BF761253 RC2-CS001

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C	7	21	3.4	482	9	AM782526	AM782526 daa94b10.x
C	8	21	3.4	508	10	BF761312	BF761312 RC2-CS001
C	9	21	3.4	557	10	B0398699	B0398699 NISC mo10
C	10	21	3.4	600	13	B0299715	B0299715 603735813
C	11	21	3.4	613	13	B0425547	B0425547 603230891
C	12	21	3.4	636	12	B066017	B066017 B066017
C	13	21	3.4	642	13	B0291718	B0291718 604164863
C	14	21	3.4	649	12	B074501	B074501 B074501
C	15	21	3.4	781	28	BH938769	BH938769 cdcg13a12
C	16	21	3.4	821	13	B0382929	B0382929 603860114
C	17	21	3.4	883	28	AZ679224	AZ679224 ENTOM57TR
C	18	21	3.4	927	28	BH135234	BH135234 ENTOM54TF
C	19	21	3.4	942	29	CNS007PK	AL067463 Drosophila1
C	20	21	3.4	1038	29	CC226751	CC226751 CH261-430
C	21	21	3.4	1101	29	CNS0022D	AL064229 Drosophila1
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C	24	20	3.2	300	9	AV109204	AV109204 AV109204
C	25	20	3.2	343	28	AQ0909076	AQ0909076 GSTC0751
C	26	20	3.2	344	28	B61289	B61289 T2109TR TAM
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C	34	20	3.2	467	10	BF871659	BF871659 QVO-ET015
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C	47	20	3.2	590	14	CB441084	CB441084 691411 MA
C	48	20	3.2	592	14	CB449568	CB449568 703779 MA
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C	51	20	3.2	601	28	BH296852	BH296852 CH230-1H1
C	52	20	3.2	612	13	BW200060	BW200060 BW200060
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C	55	20	3.2	662	14	CB442231	CB442231 595402 MA
C	56	20	3.2	671	14	CB168645	CB168645 VOT602700
C	57	20	3.2	684	14	CB421955	CB421955 595018 MA
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C	60	20	3.2	800	28	BH331842	BH331842 CH230-46N
C	61	20	3.2	826	28	BH088072	BH088072 RPI1-24-3
C	62	20	3.2	845	28	BZ113041	BZ113041 CH230-232
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C	64	20	3.2	901	28	BH154533	BH154533 ENTOD55TR
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C	66	20	3.2	904	13	B0285976	B0285976 603604304
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C	68	20	3.2	927	13	B0840226	B0840226 AGENCOURT
C	69	20	3.2	937	28	BH135779	BH135779 ENTOP81TR
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86	19	3.1	128	12	BJ368013	BJ368013	BJ368013	159	19	3.1	166	12	BJ335599	BJ335599
87	19	3.1	129	12	BJ331549	BJ331549	BJ331549	160	19	3.1	166	12	BJ336599	BJ336599
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107	19	3.1	141	12	BJ331945	BJ331945	BJ331945	180	19	3.1	168	12	BJ395523	BJ395523
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110	19	3.1	144	12	BJ393968	BJ393968	BH400869 1008038F0	183	19	3.1	169	12	BJ331978	BJ331978
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117	19	3.1	150	12	BJ365165	BJ365165	BJ365165	190	19	3.1	170	12	BJ392827	BJ392827
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123	19	3.1	160	12	BJ335867	BJ335867	BJ335867	196	19	3.1	172	12	BJ366256	BJ366256
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126	19	3.1	161	12	BJ331140	BJ331140	BJ331140	199	19	3.1	173	12	BJ335118	BJ335118
127	19	3.1	161	12	BJ331194	BJ331194	BJ331194	200	19	3.1	173	12	BJ370571	BJ370571
128	19	3.1	161	12	BJ364495	BJ364495	BJ364495	201	19	3.1	173	12	BJ371211	BJ371211
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130	19	3.1	162	12	BJ331571	BJ331571	BJ331571	203	19	3.1	173	12	BJ394939	BJ394939
131	19	3.1	162	12	BJ368293	BJ368293	BJ368293	204	19	3.1	174	12	BJ330970	BJ330970
132	19	3.1	162	12	BJ369511	BJ369511	BJ369511	205	19	3.1	174	12	BJ332872	BJ332872
133	19	3.1	163	12	BJ370590	BJ370590	BJ370590	206	19	3.1	174	12	BJ364458	BJ364458
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135	19	3.1	163	12	BJ366012	BJ366012	BJ366012	208	19	3.1	174	12	BJ367425	BJ367425
136	19	3.1	163	12	BJ394345	BJ394345	BJ394345	209	19	3.1	174	12	BJ368286	BJ368286
137	19	3.1	164	12	BJ330583	BJ330583	BJ330583	210	19	3.1	174	12	BJ369460	BJ369460
138	19	3.1	164	12	BJ331769	BJ331769	BJ331769	211	19	3.1	174	12	BJ392643	BJ392643
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140	19	3.1	164	12	BJ337019	BJ337019	BJ337019	213	19	3.1	175	12	BJ331362	BJ331362
141	19	3.1	164	12	BJ364692	BJ364692	BJ364692	214	19	3.1	175	12	BJ333327	BJ333327
142	19	3.1	164	12	BJ365835	BJ365835	BJ365835	215	19	3.1	175	12	BJ335461	BJ335461
143	19	3.1	164	12	BJ395574	BJ395574	BJ395574	216	19	3.1	175	12	BJ365995	BJ365995
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146	19	3.1	165	12	BJ331200	BJ331200	BJ331200	219	19	3.1	175	12	BJ367667	BJ367667
147	19	3.1	165	12	BJ331262	BJ331262	BJ331262	220	19	3.1	175	12	BJ369280	BJ369280
148	19	3.1	165	12	BJ331363	BJ331363	BJ331363	221	19	3.1	175	12	BJ371111	BJ371111
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226	19	3.1	176	12	B0365597	B0365597	B0366173	299	19	3.1	182	12	B0366173	B0366173
227	19	3.1	176	12	B0365855	B0365855	B0366260	300	19	3.1	182	12	B0366260	B0366260
228	19	3.1	176	12	B0365936	B0365936	B0366306	301	19	3.1	182	12	B0366306	B0366306
229	19	3.1	176	12	B0365950	B0365950	B0366938	302	19	3.1	182	12	B0366938	B0366938
230	19	3.1	176	12	B0366752	B0366752	B0369001	303	19	3.1	182	12	B0369001	B0369001
231	19	3.1	176	12	B0371362	B0371362	B0369041	304	19	3.1	182	12	B0369041	B0369041
232	19	3.1	176	12	B0394322	B0394322	B0392778	305	19	3.1	182	12	B0392778	B0392778
233	19	3.1	176	12	B0395589	B0395589	B0394214	306	19	3.1	182	12	B0394214	B0394214
234	19	3.1	176	12	B0397621	B0397621	B0394273	307	19	3.1	182	12	B0394273	B0394273
235	19	3.1	177	10	BF874439	113-ET011	B0397106	308	19	3.1	182	12	B0397106	B0397106
236	19	3.1	177	10	B0366443	B0366443	B0330300	309	19	3.1	183	12	B0330300	B0330300
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238	19	3.1	177	12	B0364928	B0364928	B0330758	311	19	3.1	183	12	B0330758	B0330758
239	19	3.1	177	12	B0365671	B0365671	B0332462	312	19	3.1	183	12	B0332462	B0332462
240	19	3.1	177	12	B0367246	B0367246	B0333087	313	19	3.1	183	12	B0333087	B0333087
241	19	3.1	177	12	B0369923	B0369923	B0333209	314	19	3.1	183	12	B0333209	B0333209
242	19	3.1	177	12	B0371212	B0371212	B0334008	315	19	3.1	183	12	B0334008	B0334008
243	19	3.1	178	12	B0330499	B0330499	B0335802	316	19	3.1	183	12	B0335802	B0335802
244	19	3.1	178	12	B0335720	B0335720	B0336200	317	19	3.1	183	12	B0336200	B0336200
245	19	3.1	178	12	B0337737	B0337737	B0339554	318	19	3.1	183	12	B0339554	B0339554
246	19	3.1	178	12	B0337894	B0337894	B0334488	319	19	3.1	183	12	B0334488	B0334488
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248	19	3.1	178	12	B0366392	B0366392	B0364764	321	19	3.1	183	12	B0364764	B0364764
249	19	3.1	178	12	B0369271	B0369271	B0365247	322	19	3.1	183	12	B0365247	B0365247
250	19	3.1	178	12	B0394438	B0394438	B0366115	323	19	3.1	183	12	B0366115	B0366115
251	19	3.1	179	12	B0330349	B0330349	B0366493	324	19	3.1	183	12	B0366493	B0366493
252	19	3.1	179	12	B0334359	B0334359	B0366507	325	19	3.1	183	12	B0366507	B0366507
253	19	3.1	179	12	B0337941	B0337941	B0366603	326	19	3.1	183	12	B0366603	B0366603
254	19	3.1	179	12	B0366757	B0366757	B0366697	327	19	3.1	183	12	B0366697	B0366697
255	19	3.1	179	12	B0367389	B0367389	B0367077	328	19	3.1	183	12	B0367077	B0367077
256	19	3.1	179	12	B0369792	B0369792	B0367511	329	19	3.1	183	12	B0367511	B0367511
257	19	3.1	179	12	B0370696	B0370696	B0367997	330	19	3.1	183	12	B0367997	B0367997
258	19	3.1	179	12	B0392176	B0392176	B0368477	331	19	3.1	183	12	B0368477	B0368477
259	19	3.1	180	12	B0332407	B0332407	B0368528	332	19	3.1	183	12	B0368528	B0368528
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263	19	3.1	181	9	A0073883	A0073883	B0371466	336	19	3.1	183	12	B0371466	B0371466
264	19	3.1	181	12	B0334700	B0334700	B0371530	337	19	3.1	183	12	B0371530	B0371530
265	19	3.1	181	12	B0337748	B0337748	B0371546	338	19	3.1	183	12	B0371546	B0371546
266	19	3.1	181	12	B0364542	B0364542	B0392862	339	19	3.1	183	12	B0392862	B0392862
267	19	3.1	181	12	B0365471	B0365471	B0393465	340	19	3.1	183	12	B0393465	B0393465
268	19	3.1	181	12	B0366366	B0366366	B0394926	341	19	3.1	183	12	B0394926	B0394926
269	19	3.1	181	12	B0366633	B0366633	B0394964	342	19	3.1	183	12	B0394964	B0394964
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271	19	3.1	181	12	B0368917	B0368917	B0332558	344	19	3.1	184	12	B0332558	B0332558
272	19	3.1	181	12	B0368932	B0368932	B0332622	345	19	3.1	184	12	B0332622	B0332622
273	19	3.1	181	12	B0371336	B0371336	B0332685	346	19	3.1	184	12	B0332685	B0332685
274	19	3.1	181	12	B0392546	B0392546	B0333838	347	19	3.1	184	12	B0333838	B0333838
275	19	3.1	181	12	B0393052	B0393052	B0333862	348	19	3.1	184	12	B0333862	B0333862
276	19	3.1	181	12	B0393213	B0393213	B0334235	349	19	3.1	184	12	B0334235	B0334235
277	19	3.1	181	12	B0393748	B0393748	B0334918	350	19	3.1	184	12	B0334918	B0334918
278	19	3.1	181	12	B0396252	B0396252	B0336089	351	19	3.1	184	12	B0336089	B0336089
279	19	3.1	182	12	B0396469	B0396469	B0337352	352	19	3.1	184	12	B0337352	B0337352
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281	19	3.1	182	12	B0331121	B0331121	B0338005	354	19	3.1	184	12	B0338005	B0338005
282	19	3.1	182	12	B0331858	B0331858	B0338184	355	19	3.1	184	12	B0338184	B0338184
283	19	3.1	182	12	B0333370	B0333370	B0339275	356	19	3.1	184	12	B0339275	B0339275
284	19	3.1	182	12	B0334293	B0334293	B0339596	357	19	3.1	184	12	B0339596	B0339596
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286	19	3.1	182	12	B0335376	B0335376	B0365505	359	19	3.1	184	12	B0365505	B0365505
287	19	3.1	182	12	B0337450	B0337450	B0365645	360	19	3.1	184	12	B0365645	B0365645
288	19	3.1	182	12	B0337539	B0337539	B0366160	361	19	3.1	184	12	B0366160	B0366160
289	19	3.1	182	12	B0337659	B0337659	B0367177	362	19	3.1	184	12	B0367177	B0367177
290	19	3.1	182	12	B0337759	B0337759	B0367291	363	19	3.1	184	12	B0367291	B0367291
291	19	3.1	182	12	B0338064	B0338064	B0369233	364	19	3.1	184	12	B0369233	B0369233
292	19	3.1	182	12	B0338786	B0338786	B0370575	365	19	3.1	184	12	B0370575	B0370575
293	19	3.1	182	12	B0338931	B0338931	B0370690	366	19	3.1	184	12	B0370690	B0370690
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296	19	3.1	182	12	B0364632	B0364632	B0397641	369	19	3.1	184	12	B0397641	B0397641

370	19	3.1	184	12	BU397720	BU397720	443	19	3.1	191	12	BU366598	BU366598
371	19	3.1	185	12	BU330519	BU330519	444	19	3.1	191	12	BU370847	BU370847
372	19	3.1	185	12	BU332198	BU332198	445	19	3.1	191	12	BU394211	BU394211
373	19	3.1	185	12	BU333004	BU333004	446	19	3.1	191	12	BU396506	BU396506
374	19	3.1	185	12	BU334810	BU334810	447	19	3.1	192	12	BU330806	BU330806
375	19	3.1	185	12	BU335871	BU335871	448	19	3.1	192	12	BU333128	BU333128
376	19	3.1	185	12	BU337281	BU337281	449	19	3.1	192	12	BU333338	BU333338
377	19	3.1	185	12	BU337752	BU337752	450	19	3.1	192	12	BU333844	BU333844
378	19	3.1	185	12	BU338952	BU338952	451	19	3.1	192	12	BU366060	BU366060
379	19	3.1	185	12	BU364290	BU364290	452	19	3.1	192	12	BU366793	BU366793
380	19	3.1	185	12	BU365770	BU365770	453	19	3.1	192	12	BU367410	BU367410
381	19	3.1	185	12	BU365972	BU365972	454	19	3.1	192	12	BU367558	BU367558
382	19	3.1	185	12	BU366056	BU366056	455	19	3.1	192	12	BU368524	BU368524
383	19	3.1	185	12	BU367596	BU367596	456	19	3.1	192	12	BU368592	BU368592
384	19	3.1	185	12	BU367794	BU367794	457	19	3.1	192	12	BU369209	BU369209
385	19	3.1	185	12	BU368151	BU368151	458	19	3.1	192	12	BU369402	BU369402
386	19	3.1	185	12	BU368339	BU368339	459	19	3.1	192	12	BU370521	BU370521
387	19	3.1	185	12	BU369162	BU369162	460	19	3.1	192	12	BU392892	BU392892
388	19	3.1	185	12	BU370728	BU370728	461	19	3.1	192	12	BU393217	BU393217
389	19	3.1	185	12	BU391762	BU391762	462	19	3.1	192	12	BU394657	BU394657
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391	19	3.1	185	12	BU393439	BU393439	464	19	3.1	192	12	BU393120	BU393120
392	19	3.1	185	12	BU393459	BU393459	465	19	3.1	193	12	BU393417	BU393417
393	19	3.1	186	12	BU393571	BU393571	466	19	3.1	193	12	BU394750	BU394750
394	19	3.1	186	12	BU330496	BU330496	467	19	3.1	193	12	BU336010	BU336010
395	19	3.1	186	12	BU331116	BU331116	468	19	3.1	193	12	BU337192	BU337192
396	19	3.1	186	12	BU332171	BU332171	469	19	3.1	193	12	BU337679	BU337679
397	19	3.1	186	12	BU333489	BU333489	470	19	3.1	193	12	BU338989	BU338989
398	19	3.1	186	12	BU335724	BU335724	471	19	3.1	193	12	BU339241	BU339241
399	19	3.1	186	12	BU338167	BU338167	472	19	3.1	193	12	BU365470	BU365470
400	19	3.1	186	12	BU356532	BU356532	473	19	3.1	193	12	BU366903	BU366903
401	19	3.1	186	12	BU366286	BU366286	474	19	3.1	193	12	BU367776	BU367776
402	19	3.1	186	12	BU366336	BU366336	475	19	3.1	193	12	BU367815	BU367815
403	19	3.1	186	12	BU367765	BU367765	476	19	3.1	193	12	BU368395	BU368395
404	19	3.1	186	12	BU368002	BU368002	477	19	3.1	193	12	BU369763	BU369763
405	19	3.1	186	12	BU368356	BU368356	478	19	3.1	193	12	BU369803	BU369803
406	19	3.1	186	12	BU368843	BU368843	479	19	3.1	193	12	BU371305	BU371305
407	19	3.1	186	12	BU370464	BU370464	480	19	3.1	193	12	BU393516	BU393516
408	19	3.1	186	12	BU393110	BU393110	481	19	3.1	193	12	BU394718	BU394718
409	19	3.1	186	12	BU395006	BU395006	482	19	3.1	193	12	BU397343	BU397343
410	19	3.1	186	12	BU395436	BU395436	483	19	3.1	194	12	BU330777	BU330777
411	19	3.1	187	12	BU332687	BU332687	484	19	3.1	194	12	BU333021	BU333021
412	19	3.1	187	12	BU332796	BU332796	485	19	3.1	194	12	BU333991	BU333991
413	19	3.1	187	12	BU333857	BU333857	486	19	3.1	194	12	BU335717	BU335717
414	19	3.1	187	12	BU334307	BU334307	487	19	3.1	194	12	BU335845	BU335845
415	19	3.1	187	12	BU364487	BU364487	488	19	3.1	194	12	BU337634	BU337634
416	19	3.1	187	12	BU367713	BU367713	489	19	3.1	194	12	BU338900	BU338900
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418	19	3.1	187	12	BU371357	BU371357	491	19	3.1	194	12	BU338950	BU338950
419	19	3.1	187	12	BU394792	BU394792	492	19	3.1	194	12	BU364635	BU364635
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421	19	3.1	188	12	BU370352	BU370352	494	19	3.1	194	12	BU365417	BU365417
422	19	3.1	189	12	BU333104	BU333104	495	19	3.1	194	12	BU365466	BU365466
423	19	3.1	189	12	BU335488	BU335488	496	19	3.1	194	12	BU365895	BU365895
424	19	3.1	189	12	BU335889	BU335889	497	19	3.1	194	12	BU366907	BU366907
425	19	3.1	189	12	BU336100	BU336100	498	19	3.1	194	12	BU367749	BU367749
426	19	3.1	189	12	BU338302	BU338302	499	19	3.1	194	12	BU367770	BU367770
427	19	3.1	189	12	BU339406	BU339406	500	19	3.1	194	12	BU368404	BU368404
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430	19	3.1	189	12	BU369840	BU369840	503	19	3.1	194	12	BU369764	BU369764
431	19	3.1	190	12	BU338084	BU338084	504	19	3.1	194	12	BU370403	BU370403
432	19	3.1	190	12	BU364625	BU364625	505	19	3.1	194	12	BU370685	BU370685
433	19	3.1	190	12	BU369722	BU369722	506	19	3.1	194	12	BU370712	BU370712
434	19	3.1	190	12	BU369727	BU369727	507	19	3.1	194	12	BU392672	BU392672
435	19	3.1	190	12	BU370274	BU370274	508	19	3.1	194	12	BU393137	BU393137
436	19	3.1	190	12	BU393185	BU393185	509	19	3.1	194	12	BU394506	BU394506
437	19	3.1	190	12	BU394209	BU394209	510	19	3.1	194	12	BU395761	BU395761
438	19	3.1	191	12	BU333947	BU333947	511	19	3.1	194	12	BU397267	BU397267
439	19	3.1	191	12	BU364393	BU364393	512	19	3.1	194	12	BU397661	BU397661
440	19	3.1	191	12	BU365233	BU365233	513	19	3.1	194	12	BU397762	BU397762
441	19	3.1	191	12	BU365680	BU365680	514	19	3.1	195	12	BU337241	BU337241
442	19	3.1	191	12	BU366242	BU366242	515	19	3.1	195	12	BU330337	BU330337

516	19	3.1	195	12	BJ330848	BJ330848	BJ330848	589	19	3.1	199	12	BJ334004	BJ334004
517	19	3.1	195	12	BJ332403	BJ332403	BJ332403	590	19	3.1	199	12	BJ335842	BJ335842
518	19	3.1	195	12	BJ332926	BJ332926	BJ332926	591	19	3.1	199	12	BJ336661	BJ336661
519	19	3.1	195	12	BJ334840	BJ334840	BJ334840	592	19	3.1	199	12	BJ366441	BJ366441
520	19	3.1	195	12	BJ364280	BJ364280	BJ364280	593	19	3.1	199	12	BJ366669	BJ366669
521	19	3.1	195	12	BJ364652	BJ364652	BJ364652	594	19	3.1	199	12	BJ366768	BJ366768
522	19	3.1	195	12	BJ365120	BJ365120	BJ365120	595	19	3.1	199	12	BJ367256	BJ367256
523	19	3.1	195	12	BJ365304	BJ365304	BJ365304	596	19	3.1	199	12	BJ391783	BJ391783
524	19	3.1	195	12	BJ365553	BJ365553	BJ365553	597	19	3.1	199	12	BJ393071	BJ393071
525	19	3.1	195	12	BJ365659	BJ365659	BJ365659	598	19	3.1	200	12	BJ332508	BJ332508
526	19	3.1	195	12	BJ365799	BJ365799	BJ365799	599	19	3.1	200	12	BJ336484	BJ336484
527	19	3.1	195	12	BJ366213	BJ366213	BJ366213	600	19	3.1	200	12	BJ336629	BJ336629
528	19	3.1	195	12	BJ366214	BJ366214	BJ366214	601	19	3.1	200	12	BJ337086	BJ337086
529	19	3.1	195	12	BJ366519	BJ366519	BJ366519	602	19	3.1	200	12	BJ337285	BJ337285
530	19	3.1	195	12	BJ366808	BJ366808	BJ366808	603	19	3.1	200	12	BJ368112	BJ368112
531	19	3.1	195	12	BJ367117	BJ367117	BJ367117	604	19	3.1	200	12	BJ370532	BJ370532
532	19	3.1	195	12	BJ367123	BJ367123	BJ367123	605	19	3.1	200	12	BJ392398	BJ392398
533	19	3.1	195	12	BJ367772	BJ367772	BJ367772	606	19	3.1	200	12	BJ392457	BJ392457
534	19	3.1	195	12	BJ369544	BJ369544	BJ369544	607	19	3.1	200	12	BJ393072	BJ393072
535	19	3.1	195	12	BJ369609	BJ369609	BJ369609	608	19	3.1	200	12	BJ396581	BJ396581
536	19	3.1	195	12	BJ369815	BJ369815	BJ369815	609	19	3.1	201	12	BJ365171	BJ365171
537	19	3.1	195	12	BJ371255	BJ371255	BJ371255	610	19	3.1	201	12	BJ368706	BJ368706
538	19	3.1	195	12	BJ390209	BJ390209	BJ390209	611	19	3.1	201	12	BJ396169	BJ396169
539	19	3.1	195	12	BJ392634	BJ392634	BJ392634	612	19	3.1	201	12	BJ396676	BJ396676
540	19	3.1	195	12	BJ393041	BJ393041	BJ393041	613	19	3.1	201	12	BJ396787	BJ396787
541	19	3.1	195	12	BJ396343	BJ396343	BJ396343	614	19	3.1	201	12	BJ396965	BJ396965
542	19	3.1	196	12	BJ330485	BJ330485	BJ330485	615	19	3.1	202	12	BJ366221	BJ366221
543	19	3.1	196	12	BJ330546	BJ330546	BJ330546	616	19	3.1	202	12	BJ367287	BJ367287
544	19	3.1	196	12	BJ333345	BJ333345	BJ333345	617	19	3.1	202	12	BJ369141	BJ369141
545	19	3.1	196	12	BJ333626	BJ333626	BJ333626	618	19	3.1	202	12	BJ370074	BJ370074
546	19	3.1	196	12	BJ364287	BJ364287	BJ364287	619	19	3.1	202	12	BJ370307	BJ370307
547	19	3.1	196	12	BJ364797	BJ364797	BJ364797	620	19	3.1	202	12	BJ392085	BJ392085
548	19	3.1	196	12	BJ365999	BJ365999	BJ365999	621	19	3.1	202	12	BJ393191	BJ393191
549	19	3.1	196	12	BJ366081	BJ366081	BJ366081	622	19	3.1	203	12	BJ044188	BJ044188
550	19	3.1	196	12	BJ369953	BJ369953	BJ369953	623	19	3.1	203	12	BJ334331	BJ334331
551	19	3.1	196	12	BJ371315	BJ371315	BJ371315	624	19	3.1	203	12	BJ334189	BJ334189
552	19	3.1	196	12	BJ391770	BJ391770	BJ391770	625	19	3.1	203	12	BJ365750	BJ365750
553	19	3.1	196	12	BJ391907	BJ391907	BJ391907	626	19	3.1	203	12	BJ368428	BJ368428
554	19	3.1	196	12	BJ392944	BJ392944	BJ392944	627	19	3.1	203	12	BJ369525	BJ369525
555	19	3.1	196	12	BJ393546	BJ393546	BJ393546	628	19	3.1	203	12	BJ370205	BJ370205
556	19	3.1	196	12	BJ394440	BJ394440	BJ394440	629	19	3.1	203	12	BJ370519	BJ370519
557	19	3.1	196	12	BJ396187	BJ396187	BJ396187	630	19	3.1	203	12	BJ395061	BJ395061
558	19	3.1	196	12	BJ396870	BJ396870	BJ396870	631	19	3.1	203	12	BJ395155	BJ395155
559	19	3.1	196	12	BJ397086	BJ397086	BJ397086	632	19	3.1	203	14	CB475867 jne112 G1	CB475867 jne112 G1
560	19	3.1	196	12	BJ334195	BJ334195	BJ334195	633	19	3.1	204	12	BJ336176	BJ336176
561	19	3.1	197	12	BJ338392	BJ338392	BJ338392	634	19	3.1	204	12	BJ364583	BJ364583
562	19	3.1	197	12	BJ365582	BJ365582	BJ365582	635	19	3.1	204	12	BJ369173	BJ369173
563	19	3.1	197	12	BJ367125	BJ367125	BJ367125	636	19	3.1	204	12	BJ369275	BJ369275
564	19	3.1	197	12	BJ370499	BJ370499	BJ370499	637	19	3.1	204	12	BJ370108	BJ370108
565	19	3.1	197	12	BJ370559	BJ370559	BJ370559	638	19	3.1	204	12	BJ395741	BJ395741
566	19	3.1	197	12	BJ370651	BJ370651	BJ370651	639	19	3.1	204	12	BJ395984	BJ395984
567	19	3.1	197	12	BJ392968	BJ392968	BJ392968	640	19	3.1	205	12	BJ365109	BJ365109
568	19	3.1	197	12	BJ397664	BJ397664	BJ397664	641	19	3.1	205	12	BJ367398	BJ367398
569	19	3.1	197	12	BJ397799	BJ397799	BJ397799	642	19	3.1	205	12	BJ396016	BJ396016
570	19	3.1	198	12	BJ327850	BJ327850	BJ327850	643	19	3.1	205	12	BJ397021	BJ397021
571	19	3.1	198	12	BJ331545	BJ331545	BJ331545	644	19	3.1	206	12	BJ334937	BJ334937
572	19	3.1	198	12	BJ333826	BJ333826	BJ333826	645	19	3.1	206	12	BJ335105	BJ335105
573	19	3.1	198	12	BJ333916	BJ333916	BJ333916	646	19	3.1	206	12	BJ335139	BJ335139
574	19	3.1	198	12	BJ334805	BJ334805	BJ334805	647	19	3.1	207	12	BJ331873	BJ331873
575	19	3.1	198	12	BJ334855	BJ334855	BJ334855	648	19	3.1	208	12	BJ367154	BJ367154
576	19	3.1	198	12	BJ335980	BJ335980	BJ335980	649	19	3.1	209	12	BJ332131	BJ332131
577	19	3.1	198	12	BJ335980	BJ335980	BJ335980	650	19	3.1	209	12	BJ339402	BJ339402
578	19	3.1	198	12	BJ335839	BJ335839	BJ335839	651	19	3.1	209	12	BJ366135	BJ366135
579	19	3.1	198	12	BJ335845	BJ335845	BJ335845	652	19	3.1	209	12	BJ369169	BJ369169
580	19	3.1	198	12	BJ336713	BJ336713	BJ336713	653	19	3.1	209	12	BJ332671	BJ332671
581	19	3.1	198	12	BJ367249	BJ367249	BJ367249	654	19	3.1	209	12	BJ393572	BJ393572
582	19	3.1	198	12	BJ367634	BJ367634	BJ367634	655	19	3.1	210	12	BJ364673	BJ364673
583	19	3.1	198	12	BJ368761	BJ368761	BJ368761	656	19	3.1	210	12	BJ367421	BJ367421
584	19	3.1	198	12	BJ370533	BJ370533	BJ370533	657	19	3.1	210	12	BJ369008	BJ369008
585	19	3.1	199	12	BJ331318	BJ331318	BJ331318	658	19	3.1	210	12	BJ370768	BJ370768
586	19	3.1	199	12	BJ332692	BJ332692	BJ332692	659	19	3.1	210	12	BJ392307	BJ392307
587	19	3.1	199	12	BJ332999	BJ332999	BJ332999	660	19	3.1	210	12	BJ392669	BJ392669
588	19	3.1	199	12	BJ333806	BJ333806	BJ333806	661	19	3.1	210	12	BJ393825	BJ393825

[illegible]

C 808	19	3.1	773	14	CB318966	CB318966	AGENCOURT	881	18	2.9	350	9	AW523261	AW523261	UT-R-BOC-
C 809	19	3.1	774	14	CA382822	662717	NC	882	18	2.9	354	10	BF349803	BF349803	RC1-RT021
C 810	19	3.1	776	28	BH463126	BH463126	BOGG30TF	883	18	2.9	350	13	BY396634	BY396634	BY396634
C 811	19	3.1	776	29	CNS04HR9	AI291294	Tetracodn	C 884	18	2.9	364	10	BG672848	BG672848	DRNALD11
C 812	19	3.1	785	13	BUE20904	BU620904	UT-H-PH1-	C 885	18	2.9	364	10	BE652069	BE652069	UT-M-NOO-
C 813	19	3.1	801	10	BF031441	BF031441	601559241	C 886	18	2.9	365	28	B23182	B23182	F2603TR
C 814	19	3.1	806	28	BH442270	BH442270	BOGF59TR	C 887	18	2.9	367	10	BF934411	BF934411	IL5-NT027
C 815	19	3.1	823	29	EX219904	EX219904	Danilo rer	C 888	18	2.9	369	28	AQ758476	AQ758476	HS-30B5_B
C 816	19	3.1	829	29	BZ607866	BZ607866	WHAAD64TR	C 889	18	2.9	373	12	BU500737	BU500737	BU500737
C 817	19	3.1	833	13	BO434630	BO434630	AGENCOURT	C 890	18	2.9	375	10	BF320009	BF320009	uz45f02.x
C 818	19	3.1	839	28	BH680156	BH680156	BOMH87TR	C 891	18	2.9	378	13	BY672199	BY672199	BY672199
C 819	19	3.1	849	28	BZ188834	BZ188834	CH230-292	C 892	18	2.9	379	9	AA717438	AA717438	UL19d01.r
C 820	19	3.1	849	28	BH492493	BH492493	BOH030TF	C 893	18	2.9	382	9	AL960941	AL960941	AL960941
C 821	19	3.1	853	29	BZ256966	BZ256966	CH230-283	C 894	18	2.9	382	9	AW528708	AW528708	UT-R-BO1-
C 822	19	3.1	858	14	CD101836	CD101836	AGENCOURT	C 895	18	2.9	385	9	AW518622	AW518622	ha37dl1.x
C 823	19	3.1	859	28	AO895230	AO895230	HS-3133_A	C 896	18	2.9	388	9	AA413495	AA413495	vc54f10.s
C 824	19	3.1	867	29	BZ689101	BZ689101	PUBK30TD	C 897	18	2.9	388	14	TI4822	TI4822	cr8264.1amb
C 825	19	3.1	871	14	CB984594	CB984594	AGENCOURT	C 898	18	2.9	394	13	BY420082	BY420082	BY420082
C 826	19	3.1	883	14	CD100941	CD100941	AGENCOURT	C 899	18	2.9	395	9	AV007103	AV007103	AV007103
C 827	19	3.1	883	28	BH134374	BH134374	ENTNX02TF	C 900	18	2.9	396	9	AA413502	AA413502	Fugu rubr
C 828	19	3.1	922	13	BU749105	BU749105	CH3#024_G	C 901	18	2.9	396	29	FR0038874	FR0038874	md97907.r1
C 829	19	3.1	922	13	BO712352	BO712352	AGENCOURT	C 902	18	2.9	397	14	M62329	M62329	md97907.r1
C 830	19	3.1	935	13	BU186626	BU186626	AGENCOURT	C 903	18	2.9	399	14	CB706708	CB706708	AMGNUNC:S
C 831	19	3.1	970	29	CC287059	CC287059	CH261-160	C 904	18	2.9	400	9	AL1240859	AL1240859	qj99f06.x
C 832	19	3.1	973	13	BO708148	BO708148	AGENCOURT	C 905	18	2.9	401	10	BF116959	BF116959	uy92h11.y
C 833	19	3.1	989	12	BM449637	BM449637	AGENCOURT	C 906	18	2.9	404	13	BY225926	BY225926	BY225926
C 834	19	3.1	993	29	CNS03CSS	AI238213	Tetracodn	C 907	18	2.9	411	28	AQ080702	CIT-HSP-2	AQ080702
C 835	19	3.1	994	13	EX415798	EX415798	BK415798	C 908	18	2.9	416	28	AQ193240	HS-30C6_B	AQ193240
C 836	19	3.1	1018	29	CC266984	CH261-184	CC266984	C 909	18	2.9	418	14	CA859907	EST634401	CA859907
C 837	19	3.1	1020	13	BQ069158	AGENCOURT	CH261-184	C 910	18	2.9	418	14	CA859907	EST634401	CA859907
C 838	19	3.1	1069	29	CC269144	CC269144	CH261-801	C 911	18	2.9	418	14	CA859907	EST634401	CA859907
C 839	19	3.1	1113	12	BM912527	BM912527	AGENCOURT	C 912	18	2.9	419	29	AG231011	Lotus_jap	AG231011
C 840	19	3.1	1134	29	BM554577	BM554577	AGENCOURT	C 913	18	2.9	420	9	AA265183	mx9e010.r	AA265183
C 841	19	3.1	1172	12	CC264061	CC264061	CH261-57B	C 914	18	2.9	421	10	BF454454	CB763220	CB763220
C 842	19	3.1	1506	13	BO923763	BO923763	AGENCOURT	C 915	18	2.9	422	14	CB763220	BE127479	BE127479
C 843	19	3.1	3621	11	BC014216	BC014216	Homo_sapi	C 916	18	2.9	425	10	BE127479	BF936030	BF936030
C 844	19	2.9	105	10	AM844373	RC2-CN005	AM844373	C 917	18	2.9	426	10	BF936030	AM520348	AM520348
C 845	18	2.9	106	12	BJ369613	BJ369613	BJ369613	C 918	18	2.9	427	9	BU070294	iml1h11.x	BU070294
C 846	18	2.9	119	12	BJ394484	BJ394484	BJ394484	C 919	18	2.9	430	13	CB792474	AMGNUNC:N	CB792474
C 847	18	2.9	169	13	BU786688	BU786688	ik78bd2.x	C 920	18	2.9	435	14	CB792474	AQ694918	AQ694918
C 848	18	2.9	169	29	CC125698	CC125698	NDU_3E9.T	C 921	18	2.9	437	28	AQ694918	BZ885362	BZ885362
C 849	18	2.9	180	12	BJ394413	BJ394413	AGENCOURT	C 922	18	2.9	437	28	AQ694918	AZ246313	RCPI-23-4
C 850	18	2.9	197	9	AI602879	AI602879	UI-R-AEO-	C 923	18	2.9	440	28	AZ246313	AI039143	AI039143
C 851	18	2.9	199	29	CC264656	CC264656	CH261-169	C 924	18	2.9	444	9	BU070294	BO073848	BO073848
C 852	18	2.9	202	14	R46919	R46919	Y148_Rat_in	C 925	18	2.9	445	13	BO073848	AQ064336	AQ064336
C 853	18	2.9	203	10	BB358883	BB358883	BB358883	C 926	18	2.9	447	28	AQ064336	BE335343	BE335343
C 854	18	2.9	215	9	AUI80215	AUI80215	AUI80215	C 927	18	2.9	449	10	BE335343	TI5226	TI5226
C 855	18	2.9	229	9	AI810783	AI810783	tuz1a09.x	C 928	18	2.9	449	13	BO073848	AQ064336	AQ064336
C 856	18	2.9	233	28	AQ425600	AQ425600	CITBI-EL-	C 929	18	2.9	449	14	TI5226	AQ064336	AQ064336
C 857	18	2.9	234	28	AQ425600	AQ425600	CITBI-EL-	C 930	18	2.9	449	28	AQ064336	AQ064336	AQ064336
C 858	18	2.9	247	28	AQ424403	AQ424403	CITBI-EL-	C 931	18	2.9	452	28	AQ064336	AQ064336	AQ064336
C 859	18	2.9	249	9	AA725958	AA725958	v085f04.r	C 932	18	2.9	455	28	AQ064336	AQ064336	AQ064336
C 860	18	2.9	254	28	AO631375	AO631375	RCPI-11-4	C 933	18	2.9	463	13	BU073888	AQ064336	AQ064336
C 861	18	2.9	254	9	AI707761	AI707761	as35b05.x	C 934	18	2.9	463	13	BU073888	AQ064336	AQ064336
C 862	18	2.9	263	14	N74637	N74637	zass5e03.x	C 935	18	2.9	464	28	AQ064336	AQ064336	AQ064336
C 863	18	2.9	303	28	BI4762	BI4762	342P5_TV_CI	C 936	18	2.9	466	9	AI276056	AM669771	AM669771
C 864	18	2.9	304	10	BE250230	BE250230	BE250230	C 937	18	2.9	467	9	AM669771	BE656423	BE656423
C 865	18	2.9	311	10	BB363779	BB363779	BB363779	C 938	18	2.9	471	10	BE656423	AZ016432	AZ016432
C 866	18	2.9	314	9	AI695002	AI695002	w45C04.x	C 939	18	2.9	474	28	AZ016432	AA542476	AA542476
C 867	18	2.9	312	9	AI072906	AI072906	UI-R-YO-m	C 940	18	2.9	475	9	AA542476	BB785439	BB785439
C 868	18	2.9	315	12	BM162759	BM162759	EST65282	C 941	18	2.9	477	10	BB785439	TA219A04P	TA219A04P
C 869	18	2.9	319	9	AM335596	AM335596	S49H12_AG	C 942	18	2.9	477	29	TA219A04P	BM169391	BM169391
C 870	18	2.9	320	9	AU282329	AU282329	AU282329	C 943	18	2.9	479	9	BM169391	AA794789	AA794789
C 871	18	2.9	323	28	BH496688	BH496688	BOGIVSITF	C 944	18	2.9	481	9	AA794789	BM165523	BM165523
C 872	18	2.9	325	28	AZ581509	AZ581509	IM0370N17	C 945	18	2.9	481	28	BM165523	W67012	W67012
C 873	18	2.9	332	9	AA004082	AA004082	mg81G06.r	C 946	18	2.9	483	13	BM165523	BM165523	BM165523
C 874	18	2.9	336	28	BH730560	BH730560	BOHVM27TR	C 947	18	2.9	483	14	W67012	BM165523	BM165523
C 875	18	2.9	342	18	H38810	H38810	YP61d06.s1	C 948	18	2.9	486	28	BH451451	CB726437	CB726437
C 876	18	2.9	342	28	AQ283991	AQ283991	RCIT11-86	C 949	18	2.9	487	10	BF761314	BF761314	BF761314
C 877	18	2.9	343	10	BB165372	BB165372	RCIT11-86	C 950	18	2.9	488	10	BF761314	BF761314	BF761314
C 878	18	2.9	344	14	N75694	N75694	YW52a02.r1	C 951	18	2.9	488	29	BZ278364	BF635240	BF635240
C 879	18	2.9	345	9	AA611334	AA611334	vm98e03.r	C 952	18	2.9	492	10	BF635240	W59478	W59478
C 880	18	2.9	347	14	H48536	H48536	YQ78c06.s1	C 953	18	2.9	493	14	W59478	W59478	W59478

C 954	18	2.9	494	9	AL385534	AL385534
C 955	18	2.9	498	28	AO871044	AO871044
C 956	18	2.9	499	14	CB712207	CB712207
C 957	18	2.9	502	14	CA927699	CA927699
C 958	18	2.9	503	9	AA645383	AA645383
C 959	18	2.9	504	9	AA108018	AA108018
C 960	18	2.9	506	9	AI475347	AI475347
C 961	18	2.9	507	28	BZ161613	BZ161613
C 962	18	2.9	508	14	R46932	R46932
C 963	18	2.9	510	28	BH766152	BH766152
C 964	18	2.9	511	14	CB222203	CB222203
C 965	18	2.9	511	28	AO615539	AO615539
C 966	18	2.9	513	12	BM901941	BM901941
C 967	18	2.9	516	10	BG691365	BG691365
C 968	18	2.9	522	9	AA553132	AA553132
C 969	18	2.9	522	10	BB867467	BB867467
C 970	18	2.9	523	12	BM420466	BM420466
C 971	18	2.9	524	12	BM248749	BM248749
C 972	18	2.9	525	9	AI083552	AI083552
C 973	18	2.9	525	29	BZ209427	BZ209427
C 974	18	2.9	526	9	AA589816	AA589816
C 975	18	2.9	529	9	AA986635	AA986635
C 976	18	2.9	529	13	B0832325	B0832325
C 977	18	2.9	530	9	AV594979	AV594979
C 978	18	2.9	533	14	CB718562	CB718562
C 979	18	2.9	534	9	AL635090	AL635090
C 980	18	2.9	535	10	BF079553	BF079553
C 981	18	2.9	536	9	AV665904	AV665904
C 982	18	2.9	536	10	BF551380	BF551380
C 983	18	2.9	536	28	A2163137	A2163137
C 984	18	2.9	537	9	AA692240	AA692240
C 985	18	2.9	538	9	AI407899	AI407899
C 986	18	2.9	538	14	CD421378	CD421378
C 987	18	2.9	540	9	AA869274	AA869274
C 988	18	2.9	540	12	BM247898	BM247898
C 989	18	2.9	541	29	TA200C070	TA200C070
C 990	18	2.9	542	12	BG969177	BG969177
C 991	18	2.9	544	28	AZ599983	AZ599983
C 992	18	2.9	545	12	BI976417	BI976417
C 993	18	2.9	545	28	AO995499	AO995499
C 994	18	2.9	545	28	AZ521396	AZ521396
C 995	18	2.9	545	28	AO527000	AO527000
C 996	18	2.9	546	13	B0833524	B0833524
C 997	18	2.9	548	10	BF079230	BF079230
C 998	18	2.9	548	12	BI499456	BI499456
C 999	18	2.9	549	10	BB669025	BB669025
C 1000	18	2.9	552	10	BF519187	BF519187

ALIGNMENTS

RESULT 1
B2862884 765 bp DNA linear GSS 18-MAR-2003
LOCUS CH240_286018.TU CHORI-240 Bos taurus genomic clone CH240_286018,
DEFINITION genomic survey sequence.
ACCESSION B2862884
VERSION B2862884.1 GI:29090289
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 765)
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,
A., Gebregorgis,E., Chen,D., Riggs,F., de Jong,P., Crawford,A.M.
and McEwan,J.C.
Bovine BAC End Sequences from Library CHORI-240
TITLE Unpublished
JOURNAL Contact: Shaying Zhao
COMMENT Department of Eukaryotic Genomics

FEATURES
source
1..765
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_286018"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTRABAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull Li Domino 993/5; CHORI-240 Bovine BAC
library (Male) produced by Pletier de Jong"
BASE COUNT 341 a 125 c 122 g 177 t
ORIGIN

Query Match 3.9%; Score 24; DB 29; Length 765;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 356 TTAATTAAATGAGTAATTAA 379
|||||
Db 142 TTAATTAAATGAGTAATTAA 165
|||||

RESULT 2
CC221787 999 bp DNA linear GSS 12-MAY-2003
LOCUS CC221787
DEFINITION CH261-92124.RM1.1 CH261 Gallus gallus genomic clone CH261-92124,
ACCESSION CC221787
VERSION CC221787.1 GI:30546360
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 999)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
TITLE Unpublished
JOURNAL Contact: Richard K. Wilson
COMMENT Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 182000 Std Error: 0.00
Class: BAC ends
High quality sequence start: 27
High quality sequence stop: 721.
FEATURES
1..999
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"

/db_xref="taxon:9031"
 /clone="CH261-92124"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTARBC2.1; Site 1: EcoRI, Site 2: EcoRI;
 CH261 Female Chicken Library - For library and clone
 ordering information: <http://www.chori.org/bacpac>"

BASE COUNT 364 a 185 c 155 g 292 t 3 others
 ORIGIN

Query Match 3.5%; Score 22; DB 29; Length 999;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 343 ACTACAAAGGTTTAAATTTA 364
 Db 838 ACTACAAAGGTTTAAATTTA 817

RESULT 3
 LOCUS C25646 151 bp mRNA linear EST 28-APR-1999
 DEFINITION C25646 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
 discoideum cDNA clone SSA869, mRNA sequence.
 ACCESSION C25646
 VERSION C25646.1 GI:2281862
 KEYWORDS EST

SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.

REFERENCE 1 (bases 1 to 151)
 Yoshino, R., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
 Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
 The Dictyostelium developmental cDNA project: generation and
 analysis of expressed sequence tags from the first-finger stage of
 development
 JOURNAL DNA Res. 5 (6), 335-340 (1998)
 MEDLINE 99156227
 PUBMED 10048482

COMMENT Contact: Hideko Urushihara
 Institute of Biological Sciences
 1-1-1 Tenoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tsukuba.ac.jp
 PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
 POLYA=No.

FEATURES
 source location/Qualifiers

1..151
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="SSA869"
 /dev_stage="sling"
 /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"

BASE COUNT 104 a 5 c 6 g 36 t
 ORIGIN

Query Match 3.4%; Score 21; DB 14; Length 151;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 370 AGTAAATTTAATATAATAA 390
 Db 96 AGTAAATTTAATATAATAA 116

RESULT 4
 BF761253/c

LOCUS BF761253 461 bp mRNA linear EST 12-JAN-2001
 DEFINITION RC2-CS0017-041000-018-f06 CS0017 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BF761253
 VERSION BF761253.1 GI:12109140
 KEYWORDS EST

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 461)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2&t2=RC2-CS0017-041000-018-f06&t3=2000-10-04&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 79
 High quality sequence stop: 460.
 location/Qualifiers

1..461
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CS0017"
 /note="Organ: colon est; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORSTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 150 a 99 c 94 g 118 t
 ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 461;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 GTATATGCTTATTTATTTAT 246
 Db 64 GTATATGCTTATTTATTTAT 44

RESULT 5
 BF761308/c
 LOCUS BF761308 462 bp mRNA linear EST 12-JAN-2001
 DEFINITION RC2-CS0017-041000-019-f11 CS0017 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BF761308
 VERSION BF761308.1 GI:12109195
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 462)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Bordin, S., Costa, P.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE
 PUBLISHED 20020663
 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/bcr/pcr/gethtml2.pl?l=RC2&t2=RC2-CS0017-041000-019-file&t3=2000-10-04&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 38
 High quality sequence stop: 461.

FEATURES
 source
 1..462
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1lb="CS0017"
 /note="Organ: colon test; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 150 a 106 c 96 g 110 t
 ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 462;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 GTATATGCTTATTTATTTAT 246
 |||||
 DB 25 GTATATGCTTATTTATTTAT 5

RESULT 6
 LOCUS BU482818 469 bp mRNA linear EST 30-NOV-2002
 DEFINITION 603847786F1 CSEQRBN22 Gallus gallus cDNA clone CHEST839K22 5', mRNA sequence.
 ACCESSION BU482818
 VERSION BU482818.1 GI:25976395
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus
 1 (bases 1 to 469)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 JOURNAL MEDLINE
 PUBLISHED 22355534
 12445392

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1..469
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST839K22"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="CSEQRBN22"
 /note="Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT 120 a 114 c 97 g 138 t
 ORIGIN

Query Match 3.4%; Score 21; DB 13; Length 469;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACAGAGAAAGCAACCCGAAA 42
 |||||
 DB 88 ACAGAGAAAGCAACCCGAAA 108

RESULT 7
 LOCUS AW782526 482 bp mRNA linear EST 30-MAR-2001
 DEFINITION da94b10.x1 Xenopus laevis tadpole stage 24 Xenopus laevis cDNA 3', mRNA sequence.
 ACCESSION AW782526
 VERSION AW782526.1 GI:7797060
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.
 1 (bases 1 to 482)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCam, R., Waterston, R. and Wilson, R.
 WashU Xenopus EST project, 1999
 Unpublished
 Contact: Sandy Clifton, Ph.D.
 WashU Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

EMAIL: est@watson.wustl.edu
 Library constructed by B. Korn PhD. and S. Henze DNA Sequencing by:
 Washington University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the RessourcenzentrumPrimatendatenbank, Berlin, Germany (web
 address: www.rzpd.de)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 419.
 Location/Qualifiers

1..482
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /sex="mixed"
 /tissue_type="whole tadpole"
 /dev_stage="stage 24"
 /lab_host="DH10B"
 /clone_1lb="Xenopus laevis tadpole stage 24"
 /note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
 Method of cloning used: directed ligation; insertcheck:
 95.8 blue and 4.2 white. Library constructed by Dr.
 Bernhard Korn and Sabine Henze. Note: This is a Xenopus
 Gene Collection (XGC) library."
 BASE COUNT 151 a 89 c 104 g 138 t
 ORIGIN

Query Match 3.4%; Score 21; DB 9; Length 482;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 156 ACGTCATTTTGAACAAATTTT 176
 |||||
 44 ACGTCATTTTGAACAAATTTT 64

RESULT 8
 LOCUS BF761312 508 bp mRNA linear EST 12-JAN-2001
 DEFINITION RC2-CS0017-041000-019-h01 CS0017 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BF761312
 VERSION BF761312.1 GI:12109199
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 508)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
 Goldmann, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.V. and
 Simpson, A.J.G.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-37064922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?pl=RC2&t2=RC2-CS0017-
 041000-019-h01&t3=2000-10-04&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 49
 High quality sequence stop: 500.

FEATURES

source

Location/Qualifiers
 1..508
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1lb="CS0017"
 /note="Organ: colon est; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORSTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 161 a 112 c 107 g 128 t
 ORIGIN

Query Match 3.4%; Score 21; DB 10; Length 508;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 226 GTATATGCTTATTATTAT 246
 |||||
 49 GTATATGCTTATTATTAT 29

RESULT 9
 LOCUS BQ398699 557 bp mRNA linear EST 22-MAY-2002
 DEFINITION NISC_mol0a05.x1 Soares NXEG Xenopus laevis cDNA clone IMAGE:5278737
 3', mRNA sequence.
 ACCESSION BQ398699
 VERSION BQ398699.1 GI:21086386
 KEYWORDS EST.
 SOURCE
 ORGANISM Xenopus laevis (African clawed frog)
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 Xenopodidae; Xenopus.
 1 (bases 1 to 557)
 NIH-XCG http://image.llnl.gov/image/html/xenopus1lb.info.shtml.
 National Institute of Child Health and Human Development, National
 Cancer Institute, Xenopus Gene Collection
 Unpublished
 JOURNAL
 COMMENT
 CONTACT: Robert Strauberg, Ph.D.
 Email: cgabbs-remail.llnl.gov
 cDNA Library Preparation: M. Bento Soares (University of Iowa)
 DNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-cGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 info@image.llnl.gov
 Plate: L1AM11704 row: A column: 10
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1..557
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:5278737"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="Soares NXEG"
 /note="Vector: pT773D-Pac (Pharmacia) with a modified
 polylinker; Site 1: NotI; Site 2: EcoRI; at strand was
 primed with a Not I - 01igo (dt) primer [5'
 TGTATCCAAATCGAAGCGGCGCGCGCAATCTTTTTTTTTTTTTTTT 3']
 , double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT773 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo
 (University of Iowa). Note: This is a Xenopus Gene

```

BASE COUNT      180 a      104 c      122 g      151 t
ORIGIN
Query Match      3.4%; Score 21; DB 13; Length 557;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      156 ACGTCATTTGAACAATTT 176
Db      |||||||||||||||||||
        26 ACGTCATTTGAACAATTT 46

RESULT 10      600 bp      mRNA      linear      EST 27-NOV-2002
BU299715      603733813F1 CSEQCHN56 Gallus gallus cDNA clone CHEST620j4 5', mRNA
LOCUS
DEFINITION
ACCESSION      BU299715
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 600)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
PUBMED
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES
source
1..600
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton line 15T"
/db_xref="taxon:9031"
/clone="CHEST620j4"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="CSEQCHN56"
/note="Organ: Small intestine; Vector: pBluescript II KS(+)
; Site_1: EcoRI; Site_2: NotI; This normalized library
was constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

BASE COUNT      158 a      148 c      145 g      149 t
ORIGIN
Query Match      3.4%; Score 21; DB 13; Length 600;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      22 ACAGAGAAAGCAACCCGAAA 42
Db      |||||||||||||||||||
        226 ACAGAGAAAGCAACCCGAAA 246

RESULT 11      613 bp      mRNA      linear      EST 29-NOV-2002
BU425547      603230891F1 CSEQRBN09 Gallus gallus cDNA clone CHEST226e23 5', mRNA
LOCUS
DEFINITION
ACCESSION      BU425547
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 613)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392
PUBMED
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES
source
1..613
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST226e23"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone.lib="CSEQRBN09"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI;
Site_2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunt-ended, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

BASE COUNT      164 a      152 c      144 g      153 t
ORIGIN
Query Match      3.4%; Score 21; DB 13; Length 613;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 ACAGAGAAAGCAACCCGAAA 42
Db      |||||||||||||||||||
        226 ACAGAGAAAGCAACCCGAAA 246

RESULT 12

```

BJ066017/c 636 bp mRNA linear EST 10-DEC-2001
 LOCUS BJ066017 NIBB Mochii normalized Xenopus tailbud library Xenopus
 DEFINITION laevis cDNA clone XL084007 5', mRNA sequence.
 ACCESSION BJ066017
 VERSION BJ066017.1 GI:17479068
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 636)
 AUTHORS Kityayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 FEATURES
 source 1..636
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XL084007"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /clone_1lb="NIBB Mochii normalized Xenopus tailbud
 library"
 BASE COUNT 182 a 135 c 122 g 195 t 2 others
 ORIGIN
 Query Match 3.4%; Score 21; DB 12; Length 636;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 156 ACGTCATTTGAACAATTTT 176
 ||||||||||||||||||
 Db 592 ACGTCATTTGAACAATTTT 572
 RESULT 13
 BU291718 642 bp mRNA linear EST 27-NOV-2002
 LOCUS BU291718 604164863F1 CSEQCCHN55 Gallus gallus cDNA clone CHEST1022m16 5',
 DEFINITION mRNA sequence.
 ACCESSION BU291718
 VERSION BU291718.1 GI:25741174
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauvia; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 642)
 AUTHORS Boardman,P.E., Sans-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.
 FEATURES
 source 1..642
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton line 15T"
 /db_xref="taxon:9031"
 /clone="CHEST1022m16"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1lb="CSEQCCHN55"
 /note="Organ: Kidney + adrenal; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer.
 Using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."
 BASE COUNT 179 a 175 c 167 g 121 t
 ORIGIN
 Query Match 3.4%; Score 21; DB 13; Length 642;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 ACAGAGAAAGCAACCCGANA 42
 ||||||||||||||||||
 Db 443 ACAGAGAAAGCAACCCGANA 463
 RESULT 14
 BU074501/c 649 bp mRNA linear EST 11-DEC-2001
 LOCUS BU074501 NIBB Mochii normalized Xenopus tailbud library Xenopus
 DEFINITION laevis cDNA clone XL090908 5', mRNA sequence.
 ACCESSION BU074501
 VERSION BU074501.1 GI:17504690
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 REFERENCE 1 (bases 1 to 649)
 AUTHORS Kityayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
 Y.
 TITLE Expressed genes in X. laevis embryo
 JOURNAL Unpublished
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 FEATURES
 source 1..649
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="XL090908"
 /tissue_type="whole embryo"
 /dev_stage="stage 25"
 /clone_1lb="NIBB Mochii normalized Xenopus tailbud
 library"

BASE COUNT 182 a 138 c 126 g 197 t 6 others
 ORIGIN

Query Match 3.4%; Score 21; DB 12; Length 649;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 156 ACGTCATTTGGAACAATTTT 176
 |||||
 Db 604 ACGTCATTTGGAACAATTTT 584

RESULT 15
 BH938769 781 bp DNA linear GSS 01-OCT-2002
 LOCUS odg3a12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION
 ACCESSION BH938769
 VERSION BH938769.1 GI:23418835
 KEYWORDS
 SOURCE
 ORGANISM
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 781)
 Delehanthy,K., Fewell,G., Fulton,L., McComble,W.R., Miner,T., Nash
 W., Rabinowicz,P.D. and Wilson,R.K.
 Whole genome shotgun reads from Brassica oleracea
 Unpublished
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.wustl.edu
 Plate: odg13 row: a column: 12
 Seq primer: -28RPPOT reverse
 Class: Shotgun
 High quality sequence start: 74
 High quality sequence stop: 511.
 Location/Qualifiers
 1..781
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_lib="B.oleracea002"
 /note="Vector: pOTw13; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear
 prep using Brassica oleracea T01000DH3 buds provided by
 Thomas Osborn at the University of Wisconsin. Genomic
 DNA was provided by Pablo Rabinowicz (CSHU) and the
 shotgun library prepared at Washington University Genome
 Sequencing Center."

BASE COUNT 232 a 212 c 120 g 216 t 1 others
 ORIGIN

Query Match 3.4%; Score 21; DB 28; Length 781;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 589 CTAATTCCTATGACAAATTAAT 609
 |||||
 Db 545 CTAATTCCTATGACAAATTAAT 565

RESULT 16
 BU382929 821 bp mRNA linear EST 28-NOV-2002
 LOCUS 603860114P1 CSEQCHN75 Gallus gallus cDNA clone CHEST870K4 5', mRNA
 DEFINITION
 ACCESSION BU382929
 VERSION BU382929.1 GI:25890930
 KEYWORDS
 EST.
 SOURCE
 Gallus gallus (chicken)

ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 821)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.O.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22355534
 MEDLINE
 PUBMED
 12445392

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 12445392

COMMENT
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST
)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 01612080930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1..821
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST870K4"
 /dev_stage="36"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN75"
 /note="Organ: trunks; Vector: pBluescript II KS(+);
 Site 1: EcoRI; Site 2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was bluntended, ligated to NotI adapters, digested with EcoRI
 , size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

BASE COUNT 217 a 226 c 222 g 156 t
 ORIGIN

Query Match 3.4%; Score 21; DB 13; Length 821;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 ACAGAGAAAGCAACCCGAAA 42
 |||||
 Db 676 ACAGAGAAAGCAACCCGAAA 696

RESULT 17
 A2679224 883 bp DNA linear GSS 14-DEC-2000
 LOCUS ENTMM377R Entamoeba histolytica Sheared DNA Entamoeba histolytica
 DEFINITION
 ENTMM377R Entamoeba histolytica Sheared DNA Entamoeba histolytica
 genomic, genomic survey sequence.
 ACCESSION A2679224
 VERSION A2679224.1 GI:11816370
 KEYWORDS
 SOURCE
 GSS.
 Entamoeba histolytica
 Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.
 1 (bases 1 to 883)
 Loftus,B., Van Aken,S. and Fraser,C.
 Determination of clone end sequences from Entamoeba histolytica
 HMI:IMS Sheared DNA library
 Unpublished
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlouf@icigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence stop: 664.
Location/Qualifiers

FEATURES

SOURCE

```
1. .883
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: pHOSt; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."
```

BASE COUNT

ORIGIN

```
384 a 340 t
77 c 82 g
```

Query Match 3.4%; Score 21; DB 28; Length 883;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 348 AAAGTTTTTAATTAAATG 368
|||||
Db 116 AAAGTTTTTAATTAAATG 136
```

RESULT 18
BH135234 927 bp DNA linear GSS 07-AUG-2001
LOCUS BH135234
DEFINITION ENTN154TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
ACCESSION BH135234
VERSION BH135234.1 GI:15094295
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
REFERENCE 1 (bases 1 to 927)
AUTHORS Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
JOURNAL HM1:IMSS sheared DNA library (2001)
COMMENT Unpublished
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlouf@icigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 27
High quality sequence stop: 592.
Location/Qualifiers

FEATURES

SOURCE

```
1. .927
```

```
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: pHOSt; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."
```

BASE COUNT

ORIGIN

```
400 a 113 g 325 t
89 c
```

Query Match 3.4%; Score 21; DB 28; Length 927;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Oy 348 AAAGTTTTTAATTAAATG 368
|||||
Db 69 AAAGTTTTTAATTAAATG 89
```

RESULT 19
CNS007PK 942 bp DNA linear GSS 03-JUN-1999
LOCUS CNS007PK/C
DEFINITION Drosophila melanogaster genome survey sequence TE03 end of BAC # BACR15G19 of RPCR-38 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL067463
VERSION AL067463.1 GI:4946027
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
REFERENCE 1 (bases 1 to 942)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Osoegawa and Aaron Mammose in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCR-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers

FEATURES

SOURCE

```
1. .942
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACR15G19"
/clone_lib="RPCR-98"
/notes="end : TE03"
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BASE COUNT 272 a 169 c 133 g 253 t 115 others
 ORIGIN

Query Match 3.4%; Score 21; DB 29; Length 942;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 504 AAACCTTTTACCATTTATTTA 524
 |||||
 Db 199 AAACCTTTTACCATTTATTTA 179

RESULT 20
 CC226751/c 1038 bp DNA linear GSS 12-MAY-2003
 LOCUS CH261-4309, Sp6.1 CH261 Gallus gallus genomic clone CH261-4309,
 DEFINITION genomic survey sequence.
 ACCESSION CC226751
 VERSION CC226751.1 GI:30553414
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1038)
 Krenitki, C., Higgsbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 TITLE Gallus gallus BAC End Reads
 JOURNAL Unpublished
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.wustl.edu
 Insert Length: 18200 Std Error: 0.00
 Seq primer: Sp6 ATTAGTGTACACATATAG
 Class: BAC ends
 High quality sequence start: 73
 High quality sequence stop: 568.
 FEATURES
 source
 1..1038
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-4309"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: PTARBAC2.1; Site 1: EcorI; Site 2: EcorI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.chori.org/bacpac"
 BASE COUNT 324 a 226 c 198 g 283 t 7 others
 ORIGIN

Query Match 3.4%; Score 21; DB 29; Length 1038;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 354 TTTTAAATTTAATGAGTAA 374
 |||||
 Db 978 TTTTAAATTTAATGAGTAA 958

RESULT 21
 CDS002YD/c 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
 DEFINITION BACR07023 of RPT-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL064229
 VERSION AL064229.1 GI:4941379
 KEYWORDS GSS.

SOURCE
 ORGANISM Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 TITLE Direct Submission
 AUTHORS Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Oseegawa and
 Aaron Mamoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPT-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 FEATURES
 source
 1..1101
 /organism="Drosophila melanogaster"
 /mol_type="Genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR07023"
 /clone_lib="RPT-98"
 /note="end : TET3"
 BASE COUNT 280 a 220 c 202 g 346 t 53 others
 ORIGIN

Query Match 3.4%; Score 21; DB 29; Length 1101;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 504 AAACCTTTTACCATTTATTTA 524
 |||||
 Db 201 AAACCTTTTACCATTTATTTA 181

RESULT 22
 A2786231/c 165 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0031D07R Mouse 10kb plasmid UUC21M library Mus musculus genomic
 DEFINITION clone UUCG2M0031D07 R, genomic survey sequence.
 ACCESSION A2786231
 VERSION A2786231.1 GI:12923783
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 165)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished
 JOURNAL Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 COMMENT

Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: D column: 07
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 165.
 Location/Qualifiers

FEATURES

source

```
1..165
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0031D07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

BASE COUNT

53 a 24 c 36 g 52 t

ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 165;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 TGCTTAATACAGATAGTA 573
 DB 20 TGCTTAATACAGATAGTA 1

RESULT 23

A0088456/c

LOCUS 1 (bases 1 to 296)
 DEFINITION HS_2208 B1.D03 MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=H, genomic survey sequence.

ACCESSION A0088456
 VERSION A0088456.1 GI:3457367
 KEYWORDS GSS.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 296)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

COMMENT

10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 2208 row: H column: 5
 Class: BAC ends
 High quality sequence stop: 296.
 Location/Qualifiers

FEATURES

source

```
1..296
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2208 Col=5 Row=H"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC clones in E-Coli DH10B"
```

BASE COUNT

126 a 45 c 42 g 83 t

ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 296;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 ACAAGGTTTAAATTAA 365
 DB 181 ACAAGGTTTAAATTAA 162

RESULT 24

AV109204

LOCUS AV109204 300 bp mRNA linear EST 28-JUN-1999
 DEFINITION AV109204 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA

ACCESSION- AV109204.1 GI:5256752
 VERSION AV109204.1
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 300)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AKehira,S., Akiyama,K., Ozawa,Y., Kono,H., Itoh,M., Aizawa,K., Akiyama,S., Shibata,Y., Fukuda,S., Fukuishi,Y., Funayama,T., Hara A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Suganara Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tomihata,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs
 JOURNAL Unpublished
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp
 Thermostabilization and thermocatalytic activation of thermostable enzymes by thermostabilization and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES

source

```
1..300
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2600001A05"
```


JOURNAL
COMMENT

Unpublished
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@atc@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 310
POLYA=No.

FEATURES

source location/Qualifiers

1. 357
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Floral-Induced Meristem 1 (FM1)"
/note="Organ: Floral-Induced meristems; Vector: pBluescript II from lambda Zap II; Site_1: XhoI; Site_2: EcoRI; mature plants were placed in a growth chamber for 15 days with 16 hr darkness and 8 hr light (flowering is induced by short-day conditions); 16 days after being returned to the greenhouse under natural long days during late April/early May, meristems were harvested. The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 55 a 137 c 98 g 66 t 1 others

ORIGIN

Query Match 3.2%; Score 20; DB 10; Length 357;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 110 CTGCAGCAGGATCTGGGG 129
|||||
Db 236 CTGCAGCAGGATCTGGGG 217

RESULT 28
AW779697/c 364 bp mRNA linear EST 12-MAY-2000
LOCUS hm84a01.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3034536 3',
DEFINITION mRNA sequence.

ACCESSION AW779697

VERSION AW779697.1 GI:7794300

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 364)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

REFERENCE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

COMMENT

Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN, send email to:
info@image.lnl.gov
Seq primer: 40UP from Gibco.

FEATURES

source

1. 364
/organism="Homo sapiens"

BASE COUNT

85 a 85 c 76 g 118 t

ORIGIN

Query Match 3.2%; Score 20; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 183 TATTTTACAGATCATTTTC 202
|||||
Db 77 TATTTTACAGATCATTTTC 58

RESULT 29
AI503250/c 402 bp mRNA linear EST 11-MAR-1999

LOCUS vm12f01.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
DEFINITION IMAGE:1020985 3', mRNA sequence.

ACCESSION AI503250

VERSION AI503250.1 GI:4401101

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 402)

REFERENCE

Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rittler
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999

Unpublished
Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:571761

This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 401.

FEATURES

source

1. 402
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1020985"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: ~5'
adaptor sequence: 5' GAATTCGGACGACG 3' ~3' adaptor
sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' "

BASE COUNT

124 a 74 c 76 g 128 t

Query Match 3.2%; Score 20; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 TGCTTAATACGAGATAGTA 573
|||||
Db 263 TGCTTAATACGAGATAGTA 244

RESULT 30

AV683576 403 bp mRNA linear EST 16-JAN-2002

DEFINITION AV683576 GKC Homo sapiens cDNA clone GKCAF12 5', mRNA sequence.

AV683576
VERSION AV683576.1 GI:10285439

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 403)
Xu X., Huang J., Xu Z., Qian B., Zhu Z., Yan Q., Cai T., Zhang X.,
Xiao H., Qu J., Liu F., Huang Q., Cheng Z., Li N., Du J., Hu W.,
Shen K., Lu G., Fu G., Zhong W., Xu S., Gu W., Huang W., Zhao X.,
Hu G., Gu J., Chen Z., and Han Z.

TITLE

Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

MEDLINE 21625106
PUBMED 11752456

COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.
Location/Qualifiers

FEATURES
1.403
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCAF12"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_id="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 106 a 81 c 99 g 117 t
ORIGIN

Query Match 3.2%; Score 20; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 CTAATTCATGACAAATTA 608
|||||
Db 166 CTAATTCATGACAAATTA 185

RESULT 31
BM200515 403 bp mRNA linear EST 05-NOV-2002

DEFINITION BM200515 Nori Satoh unpublished cDNA library, cleaving embryo Ciona
intestinalis cDNA clone c1c1074007 5', mRNA sequence.

ACCESSION BM200515
VERSION BM200515.1 GI:24614944

KEYWORDS EST.
SOURCE Ciona intestinalis

ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 403)
Satou, Y., Shin, I. T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2002c)

AUTHORS

TITLE

JOURNAL

COMMENT Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@scidian.zool.kyoto-u.ac.jp.

FEATURES
1.403
Location/Qualifiers

source
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="c1c1074007"
/tissue_type="whole body"
/dev_stage="cleaving embryo"
/clone_id="Nori Satoh unpublished cDNA library, cleaving
embryo"
BASE COUNT 112 a 49 c 76 g 158 t 8 others
ORIGIN

Query Match 3.2%; Score 20; DB 13; Length 403;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 CATTGGAACAAATTTCTA 179
|||||
Db 136 CATTGGAACAAATTTCTA 155

RESULT 32

AV806526 410 bp mRNA linear EST 29-MAR-2002

DEFINITION AV806526 RAP19 Arabidopsis thaliana cDNA clone RAP109-46-P03 3',
mRNA sequence.

AV806526
VERSION AV806526.1 GI:19840511

KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 410)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rcc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda PUC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This

Query Match 3.2%; Score 20; DB 10; Length 467;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 ATGCTTATTTATTTATGTT 249
 |||||
 408 ATGCTTATTTATTTATGTT 389

RESULT 35
 A0052026 481 bp DNA linear GSS 20-APR-1999
 LOCUS RPCI11-49024.TV RPCI-11 Homo sapiens genomic clone RPCI-11-49024,
 DEFINITION genomic survey sequence.
 ACCESSION A0052026
 VERSION A0052026.1 GI:3349063
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 481)
 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
 Venter,J.C.
 Title Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 JOURNAL Unpublished
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@edlong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (http://ciresgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Class: BAC ends.
 Location/Qualifiers
 1..481
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GBS:7518791"
 /db_xref="taxon:9606"
 /clone="RPCI-11-49024"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACg3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPCI11 Human Male BAC library"

BASE COUNT 169 a 92 c 120 g 100 t

ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 481;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 251 CTCAGAGATGCTATTTTA 270
 |||||
 394 CTCAGAGATGCTATTTTA 413

RESULT 36
 A2450611 482 bp DNA linear GSS 04-OCT-2000
 LOCUS 1M0249K19F Mouse 10kb plasmid UNGC1M library Mus musculus genomic
 DEFINITION clone UNGC1M0249K19 F, genomic survey sequence.
 ACCESSION A2450611
 VERSION A2450611.1 GI:10605573
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 482)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0249 row: K column: 19
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 482.
 Location/Qualifiers
 1..482
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UNG1M0249K19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UNGC1M library"
 /note="Vector: pMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD43 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 137 a 99 c 87 g 159 t

ORIGIN

Query Match 3.2%; Score 20; DB 28; Length 482;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 233 CTTTATTTATTTATGTTGCT 252
 |||||
 399 CTTTATTTATTTATGTTGCT 418

RESULT 37
 B2861579 483 bp DNA linear GSS 18-MAR-2003
 LOCUS CH240_258J20.TV CHORI-240 Bos taurus genomic clone CH240_258J20,
 DEFINITION genomic survey sequence.
 ACCESSION B2861579
 VERSION B2861579.1 GI:29088984

KEYWORDS
GSS.
Bos taurus (cow)
SOURCE
Bos taurus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS
1 (bases 1 to 483)
Zha, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregiorgis, E., Chen, D., Riggs, F., de Jong, P., Crawford, A.M. and McEwan, J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished
TITLE
JOURNAL
COMMENT
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pjejong@tigr.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.
Plate: 258 row: J column: 20
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..483
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_258j20"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

BASE COUNT
ORIGIN
184 a 69 c 73 g 157 t

Query Match 3.2%; Score 20; DB 29; Length 483;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 159 TCATTTCGAACAAATTTCT 178
|||||
24 TCATTTCGAACAAATTTCT 43

RESULT 38
BP889646 491 bp mRNA linear EST 25-APR-2001
DEFINITION 289193 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BP889646
VERSION BP889646.1 GI:12281104
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS
1 (bases 1 to 491)
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Perle, G., Holt, I., Karaymcheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.

TITLE
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL
MEDLINE 21180013
PUBMED 11282978
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@meat.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR primers
FORWARD: AGGAACGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 94 row: M column: 24
Seq primer: ATTAGGTGACACTATG.
Location/Qualifiers
1..491
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

BASE COUNT
ORIGIN
151 a 78 c 96 g 166 t

Query Match 3.2%; Score 20; DB 10; Length 491;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 348 AAAGCTTTTAAATTTAAAT 367
|||||
381 AAAGCTTTTAAATTTAAAT 400

RESULT 39
BP956275/c 498 bp mRNA linear EST 22-JAN-2001
DEFINITION QV2-NN0045-211100-495-F02 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP956275
VERSION BP956275.1 GI:12373550
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 498)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
TITLE
JOURNAL
MEDLINE 2020263
PUBMED 10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV2&t=QV2-NN0045-21100-495-502&t3=2000-11-21&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 498.
 Location/Qualifiers

FEATURES

source

```

1..498
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN0045"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      178 a      68 c      92 g      160 t
ORIGIN

```

Query Match
 Best Local Similarity 100.0%; Score 20; DB 10; Length 498;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 AACCAATTTTCTACTATATTT 187
 |||||
 Db 373 AACCAATTTTCTACTATATTT 354

RESULT 40

BE721612

LOCUS BE721612 498 bp mRNA linear EST 25-APR-2001
 DEFINITION 189200 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BE721612
 VERSION BE721612.1 GI:10122908
 KEYWORDS EST.

SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 498)
 Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
 Perle,G., Holt,I., Karaycheva,S., Liang,F., Quackenbush,J. and
 Keele,J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)

AUTHORS

TITLE

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

JOURNAL

MEDLINE

PUBMED

11282978

Contact: Smith TPJ

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -mismatch 12 options.

PCR primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTCACAGTCACGACG

Plate: 40 row: K column: 12

Seq primer: ATTTAGGTGACACTATAG.

FEATURES

Location/Qualifiers

1..498

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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPOR6; Site_1: NotI; Site_2: SalI; library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
BASE COUNT      157 a      90 c      89 g      162 t
ORIGIN

```

Query Match
 Best Local Similarity 100.0%; Score 20; DB 10; Length 498;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 AAGGTTTTTAATTAAAT 367
 |||||
 Db 137 AAGGTTTTTAATTAAAT 156

Search completed: October 8, 2003, 07:52:03
 Job time : 1984 secs